

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 00:16:06 ; Search time 467 Seconds  
(without alignments)  
10599.341 Million cell updates/sec

Title: US-09-913-858a-1

Perfect score: 2198

Sequence: 1 actaactcaacgctgatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N\_Geneseq\_101002:\*
- 1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*
  - 2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*
  - 3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*
  - 4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*
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  - 11: /SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*
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  - 19: /SID52/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*
  - 20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*
  - 21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*
  - 22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*
  - 23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*
  - 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2198	100.0	2198	21	AAA97937
2	661.6	30.1	1982	21	AAC39529
3	209.4	9.5	2069	22	AAF84907
4	209.4	9.5	2124	22	AAF84910
5	209.4	9.5	2165	22	AAF84913
6	209.4	9.5	2232	22	AAF84916
7	209.4	9.5	2808	22	AAF84906
8	209.4	9.5	2863	22	AAF84909
9	209.4	9.5	2904	22	AAF84912

10	209.4	9.5	2971	22	AAF84915
11	209.4	9.5	3714	22	RAF84905
12	209.4	9.5	3775	24	AD38881
13	105	4.8	105	21	AA97938
14	84.2	3.8	287	24	ABL78406
15	50	2.3	1461	21	AA40119
16	49.2	2.2	676	22	AA541344
17	49.2	2.2	1328	24	ABK11711
18	49.2	2.2	1479	24	ABA05334
19	49.2	2.2	2557	24	ABA05333
20	47.6	2.2	398	22	AAF64428
21	47	2.1	34769	22	AA546775
22	46.6	2.1	34769	22	AA546774
23	46	2.1	5931	22	AA546703
24	45.8	2.1	6136	24	ABK40042
25	45	2.0	612	22	AAH71471
26	44.8	2.0	9814	24	ABK31429
27	44.2	2.0	10020	24	ABL34293
28	44.2	2.0	12405	22	AA545330
29	44.2	2.0	12405	24	AA561143
30	44.2	2.0	12405	24	AA561143
31	43.6	2.0	626	23	ABV60941
32	43.6	2.0	2036	21	AAZ92672
33	43.6	2.0	2170	21	AAZ92672
34	43.6	2.0	113515	24	ABL34175
35	43.4	2.0	5857	24	AA563347
36	43.2	2.0	2676	21	AAZ92647
37	43.2	2.0	2822	21	AAZ92646
38	43	2.0	10377	24	ABL34221
39	42.6	1.9	9652	24	ABL32908
40	42.4	1.9	1465	21	AAC40055
41	42.4	1.9	1563	21	AAC41754
42	42.2	1.9	626	23	ABV60941
43	41	1.9	1373	21	AAZ77739
44	41	1.9	4063	21	AAF18226
45	41	1.9	5593	24	ABL33161

ALIGNMENTS

RESULT 1

AAA97937

ID AAA97937 standard; DNA; 2198 BP.

XX AAA97937;

AC AAA97937;

DT 26-JAN-2001 (first entry)

XX 1

DE Mung bean alpha 1,3-fucosyltransferase DNA.

XX alpha 1,3-fucosyltransferase; plant; mung bean; glycoprotein; insect;

XX G1CNC-alpha1,3-fucosyl transferase; ds.

OS Phaseolus aureus.

XX WO200049153-A1.

PN 24-AUG-2000.

XX 17-FEB-2000; 2000WO-AT00040.

PF 18-FEB-1999; 99AT-0000270.

PR (ALTM/ ALTMA F.

XX Altman F;

XX WPI; 2000-549274/50.

DR P-PSDB; AAB10713.

XX DNA encoding plant G1CNC-alpha-1,3-fucosyl transferase, useful for

XX recombinant production of the enzyme and recombinant glycoprotein

PT

## RESULT 2

US-09-878-574-7836  
 : Sequence 7836, Application US/09878574  
 : Patent No. US20020110548A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Byrum, Joseph R.  
 : APPLICANT: La Rosa, Michael D.  
 : APPLICANT: Thompson, Michael D.  
 : TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 : FILE REFERENCE: 38-21(15401)B  
 : CURRENT APPLICATION NUMBER: US/09/878,574  
 : PRIOR FILING DATE: 2001-12-21  
 : CURRENT FILING DATE: 09/333,535  
 : PRIOR FILING DATE: 1999-06-14  
 : NUMBER OF SEQ ID NOS: 15775  
 : SEQ ID NO 7836  
 : LENGTH: 273  
 : TYPE: DNA  
 : ORGANISM: Glycine max  
 : OTHER INFORMATION: Clone ID: 701100402H1  
 US-09-878-574-7836

Query Match 3.8%; Score 83.4; DB 10; Length 273;  
 Best Local Similarity 79.4%; Pred. No. 2.5e-13;  
 Matches 112; Conservative 0; Mismatches 26; Indels 3; Gaps 1;  
 QY 984 CCTGATGGAGAGTCAACAAAGTGAAGCCCTGAAGCACTACAAATTTAGCTTAGCGTT 1043  
 DB 1 CCTGATGGAGAGTGAACAAAGTGAAGCCCTGAAGCACTACAAATTTAGCTTAGCGTT 60  
 QY 1044 TGAATATTCGAATGAGGAAGATTATGTAACCTGAAAAAT---TCTTCCAATCCCTTTGTGC 1100  
 DB 61 TGAGAATTCCTAGCGATGATAGTAAGTAAGTCTGAAATGCTGTACATGCCATTTGTTAC 120  
 QY 1101 TGAAGTCTCCCTGGTGT 1121  
 DB 121 TGGATCAAGGTGTGGTGT 141

## RESULT 3

US-09-918-995-2051  
 : Sequence 2051, Application US/09918995  
 : Publication No. US20030073623A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Hyseq, Inc.  
 : TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 : FILE REFERENCE: 20411-756  
 : CURRENT APPLICATION NUMBER: US/09/918,995  
 : PRIOR FILING DATE: 2001-07-30  
 : PRIOR APPLICATION NUMBER: US/09/235,076  
 : NUMBER OF SEQ ID NOS: 38054  
 : SOFTWARE: FastSeq for Windows Version 3.0  
 : SEQ ID NO 2051  
 : LENGTH: 477  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : NAME/KEY: misc\_feature  
 : LOCATION: (1)...(477)  
 : OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-2051

Query Match 2.2%; Score 49.2; DB 9; Length 477;  
 Best Local Similarity 49.2%; Pred. No. 0.0017;  
 Matches 129; Conservative 0; Mismatches 133; Indels 0; Gaps 0;  
 QY 1007 TGAAGCCCTGAAGCACTACAAATTTAGCTTAGCGTTTGAATTCGAATGAGAAGATT 1066  
 DB 75 TGGCTTTCTTGTCCCGCTATAAGTCCACTTGGCCCTGGAATATGCCATCTGTAACCACT 134

QY 1067 ATGTAACGTAAAAATCTTCCAATCCCTTCTGCTGCAACTGCTCCTGCTGCTGCTGCTG 1126  
 DB 135 ACATGACAGAAAAATCTGCGGTCCCATGACACCTGGCGCTGTGCGCGGTGACCCGGTT 194  
 QY 1127 CTCCTCAATATTCAGGACTTTGCTCCTTCTCCTGCTGCTCAATTTTACATATTAAGAGATAG 1186  
 DB 195 CTCCTCTGTGAGGAGCTGGATGCCGAACAATCACTCCGCTCATCTGATGATGATTTTG 254  
 QY 1187 AGGATGTTGACTCTGTTGCAAAAGACCATGAGATATCTAGCAGAAAAATCCGAAGCATATA 1246  
 DB 255 AGTCTCTCAGCAAGCTGCAGAGTTTATTGACTTTCTGCAACAAGAATGATGAGGAGTATA 314  
 QY 1247 ATCAATCATTCAGGTGCAAGTA 1268  
 DB 315 TGAATACCTGGCATACAACA 336

## RESULT 4

US-09-960-352-12673/C  
 : Sequence 12673, Application US/09960352  
 : Patent No. US20020137139A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Warren, Wesley C.  
 : APPLICANT: Tao, Nengping  
 : APPLICANT: Byatt, John C.  
 : APPLICANT: Mathalagan, Nagappan  
 : TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
 : FILE REFERENCE: 16511.006/37-21(10298)C  
 : CURRENT APPLICATION NUMBER: US/09/960,352  
 : CURRENT FILING DATE: 2001-09-24  
 : NUMBER OF SEQ ID NOS: 15112  
 : SEQ ID NO 12673  
 : LENGTH: 277  
 : TYPE: DNA  
 : ORGANISM: Bos taurus  
 : OTHER INFORMATION: Clone ID: 54-LIB8058-039-01-K1-F10  
 US-09-960-352-12673

Query Match 1.9%; Score 41.2; DB 10; Length 277;  
 Best Local Similarity 55.6%; Pred. No. 0.21;  
 Matches 79; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
 QY 2057 TTACTTCATGTTGTTTGTGATGATCTCGAGCTTTTATGCTGCAACTGCTCCTGCTGTT 2116  
 DB 258 TTTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 199  
 QY 2117 TTGAGCACCTGTTTATGCTTCAGTGTACTGTCAGTGTGCTCCAGTGGTTATCGTTTTCACCTCTAAA 2176  
 DB 198 TAAAAATTTTCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 139  
 QY 2177 AAAAAAAAAAAAAAAAAAAAAA 2198  
 DB 138 AAAAAAAAAAAAAAAAAAAAAA 117

## RESULT 5

US-09-925-301-133  
 : Sequence 133, Application US/09925301  
 : Patent No. US20020052308A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Rosen et al.  
 : TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 : FILE REFERENCE: PA106  
 : CURRENT APPLICATION NUMBER: US/09/925,301  
 : CURRENT FILING DATE: 2001-08-10  
 : PRIOR APPLICATION NUMBER: PCT/US00/05882  
 : PRIOR FILING DATE: 2000-03-08  
 : PRIOR APPLICATION NUMBER: 60/124,270  
 : PRIOR FILING DATE: 1999-03-12  
 : NUMBER OF SEQ ID NOS: 1694  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 133

production -

Claim 1: Page 35-36; 72pp: German.

This invention describes a novel DNA molecule (I), encoding a plant protein with fucosyl transferase activity, GlcNAc- $\alpha$ 1,3-fucosyl transferase. The methods and DNA sequences are useful for production of recombinant GlcNAc- $\alpha$ 1,3-fucosyltransferase. The enzyme is useful for the production of recombinant human glycoproteins, which are especially useful in medical applications and pharmaceutical compositions. (I) can be used as a probe to select GlcNAc- $\alpha$ 1,3-fucosyltransferase coding sequences in a sample, especially from plants or insects. This sequence encodes the mung bean (*Phaseolus aureus*)  $\alpha$ 1,3-fucosyltransferase protein described in the method of the invention.

Sequence 2198 BP; 595 A; 412 C; 518 G; 673 T; 0 other;

Query Match 100.0%; Score 2198; DB 21; Length 2198;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACTAACTCAACAGCTGCTATTTCTTTTCTTTTCAGGAAACCATCCACCCATAACACAA 60  
 DB 1 ACTAACTCAACAGCTGCTATTTCTTTTCTTTTCAGGAAACCATCCACCCATAACACAA 60

OY 61 AAAAAACAACAGCAGCTGCTGTTTTTTATCGTCTTTTCTTTTAAACAAGCACCCCA 120  
 DB 61 AAAAAACAACAGCAGCTGCTGTTTTTTATCGTCTTTTCTTTTAAACAAGCACCCCA 120

OY 121 TCATGGAATCGTCTCATACGCCAAATTTTCCATTTCCCTTTTGATTTTATGTTATTT 180  
 DB 121 TCATGGAATCGTCTCATACGCCAAATTTTCCATTTCCCTTTTGATTTTATGTTATTT 180

OY 181 TCGGAAATTCGGAGTTGGGGGCCAATGAATGATGGCTCTGTGACGAATCTTCGAGGC 240  
 DB 181 TCGGAAATTCGGAGTTGGGGGCCAATGAATGATGGCTCTGTGACGAATCTTCGAGGC 240

OY 241 TCGAGACAGATGGGCCAACAGACGTTACCCGTTTGGCTCCGGGAGGCAACCCA 300  
 DB 241 TCGAGACAGATGGGCCAACAGACGTTACCCGTTTGGCTCCGGGAGGCAACCCA 300

OY 301 AAGAGAAATGGAGCAATCTAATGCTCTTTGTTGGCCCTTGTGTCATCGCGGAGATC 360  
 DB 301 AAGAGAAATGGAGCAATCTAATGCTCTTTGTTGGCCCTTGTGTCATCGCGGAGATC 360

OY 361 CGCTTTCTGGGTAGTTGGATATGGCCAAAACGCCCATGGTTGACTCCCTCGCTGAC 420  
 DB 361 CGCTTTCTGGGTAGTTGGATATGGCCAAAACGCCCATGGTTGACTCCCTCGCTGAC 420

OY 421 TTCTTTACCGCTCTCGAGCGGCTGTTGAAGGTGACGATTTGGGGTTGGGTTGGTGGCT 480  
 DB 421 TTCTTTACCGCTCTCGAGCGGCTGTTGAAGGTGACGATTTGGGGTTGGGTTGGTGGCT 480

OY 481 TCTGATCGGAATCTGAATCGTATAGTTGTGAGGAATGTTGGAGAGGAGGATGCTGTC 540  
 DB 481 TCTGATCGGAATCTGAATCGTATAGTTGTGAGGAATGTTGGAGAGGAGGATGCTGTC 540

OY 541 ACGTATTCGAGGGGCTTTTCCAAAGAGCTATTTTGTGTTCTGAGCTGATCAGAGTGG 600  
 DB 541 ACGTATTCGAGGGGCTTTTCCAAAGAGCTATTTTGTGTTCTGAGCTGATCAGAGTGG 600

OY 601 AAGTCGTGTTCCGTTGGATGTAATTTGGGTTTACTGGGGATAGAAAGCCAGATGCCCA 660  
 DB 601 AAGTCGTGTTCCGTTGGATGTAATTTGGGTTTACTGGGGATAGAAAGCCAGATGCCCA 660

OY 661 TTTGGGTTTACCTCAACCAAGTGGACAGCTAGCATTCCTGCGGATCAATGGAAATCAGCAGAA 720  
 DB 661 TTTGGGTTTACCTCAACCAAGTGGACAGCTAGCATTCCTGCGGATCAATGGAAATCAGCAGAA 720

OY 721 TACTATCTGAGAACAAATATTGCCATGGCAAGACGGAGGATATACATCGTGAATGACA 780  
 DB 721 TACTATCTGAGAACAAATATTGCCATGGCAAGACGGAGGATATACATCGTGAATGACA 780

OY 781 ACCAGTCTATCTTCGGATGTTCTCTGTTGGATATTTTTCATGGCTGAGTATGATGATG 840  
 DB 781 ACCAGTCTATCTTCGGATGTTCTCTGTTGGATATTTTTCATGGCTGAGTATGATGATG 840

OY 841 GCACCAGTGCAGCGCAAAACCTGAAGCTGCTCTTGCAGCTGCTTTTCATTTCCAAATTTGCTG 900  
 DB 841 GCACCAGTGCAGCGCAAAACCTGAAGCTGCTCTTGCAGCTGCTTTTCATTTCCAAATTTGCTG 900

OY 901 GCTCGAAATTTCCCGTTGCAAGCTCTTGAAGCCCTTTGAAATATCAACATCAAAATTTG 960  
 DB 901 GCTCGAAATTTCCCGTTGCAAGCTCTTGAAGCCCTTTGAAATATCAACATCAAAATTTG 960

OY 961 TCTATGTTGTTGTCACAGAACCTGATGGAAGAGTGAACAAAGTGAAGCCCTGAAG 1020  
 DB 961 TCTATGTTGTTGTCACAGAACCTGATGGAAGAGTGAACAAAGTGAAGCCCTGAAG 1020

OY 1021 CACTACAAATTTAGCTTTAGGCTTTGAAATTTGCAATGAGGAAGATTTGTAACCTGAAAAA 1080  
 DB 1021 CACTACAAATTTAGCTTTAGGCTTTGAAATTTGCAATGAGGAAGATTTGTAACCTGAAAAA 1080

OY 1081 TTCTTCCAAATCCCTGTTGCTGGAACCTGCTGCTGCTGTTGTTGGTCTCCAAATTTTCAG 1140  
 DB 1081 TTCTTCCAAATCCCTGTTGCTGGAACCTGCTGCTGCTGTTGTTGGTCTCCAAATTTTCAG 1140

OY 1141 GACTTTGCTCTCTCTCTCTGTTTACATTTTACATATTTAAAGAGATAGAGATGTTGAGTCT 1200  
 DB 1141 GACTTTGCTCTCTCTCTCTGTTTACATTTTACATATTTAAAGAGATAGAGATGTTGAGTCT 1200

OY 1201 GTTCAAGACCATGAGATATCTAGCAGAAAAATCCCGAAGCATATATCAATCATTTGAGG 1260  
 DB 1201 GTTCAAGACCATGAGATATCTAGCAGAAAAATCCCGAAGCATATATCAATCATTTGAGG 1260

OY 1261 TGGAGTATGAGGCTCTGCTGCTCTTCAAGGCCCTTGTGATATGCGAGCTGTGCTAT 1320  
 DB 1261 TGGAGTATGAGGCTCTGCTGCTCTTCAAGGCCCTTGTGATATGCGAGCTGTGCTAT 1320

OY 1321 TCATCTGCTGCTCTCTCTCTGCTTCAAGGCCCTTGTGATATGCGAGCTGTGCTAT 1380  
 DB 1321 TCATCTGCTGCTCTCTCTCTGCTTCAAGGCCCTTGTGATATGCGAGCTGTGCTAT 1380

OY 1381 CCAAGCTTTAAGAGACGCTCTTGCAGAACCTGAGAGGCCAGAACCCGTATATCATATC 1440  
 DB 1381 CCAAGCTTTAAGAGACGCTCTTGCAGAACCTGAGAGGCCAGAACCCGTATATCATATC 1440

OY 1441 TATGTCAGAGAAAGGGAAGGTTTGAGATGGAGTCCATTACCTAGCTAGCTAGCAATTTA 1500  
 DB 1441 TATGTCAGAGAAAGGGAAGGTTTGAGATGGAGTCCATTACCTAGCTAGCTAGCAATTTA 1500

OY 1501 ACTCTGAATGCTGGAAGGCTGCTGTTGTTTGAAGTTTACATCCCTGAATCTTGTGCTCT 1560  
 DB 1501 ACTCTGAATGCTGGAAGGCTGCTGTTGTTTGAAGTTTACATCCCTGAATCTTGTGCTCT 1560

OY 1561 GTATGGAAGACTGAAGGCCCTGAAGTTATAGAGGGGGAGTGCTTTTAAACTCTACAAA 1620  
 DB 1561 GTATGGAAGACTGAAGGCCCTGAAGTTATAGAGGGGGAGTGCTTTTAAACTCTACAAA 1620

OY 1621 ATATACCAATTTGGCTTGACACAGACAGACAGCTCTTTATACCTCAGCTTCAAAAGTGTAT 1680  
 DB 1621 ATATACCAATTTGGCTTGACACAGACAGACAGCTCTTTATACCTCAGCTTCAAAAGTGTAT 1680

OY 1681 GCTGATTTACAGGACTCAGCTTTGGAGAACAAATCTCTGTCACAAAGTTTGAAGTCAATTTTGTG 1740  
 DB 1681 GCTGATTTACAGGACTCAGCTTTGGAGAACAAATCTCTGTCACAAAGTTTGAAGTCAATTTTGTG 1740

OY 1741 TAGCATCCGCTAAATGCTACCTGCTCTACCTGAATTTAGCTTACCTAGCTAGCAGCTA 1800  
 DB 1741 TAGCATCCGCTAAATGCTACCTGCTCTACCTGAATTTAGCTTACCTAGCTAGCAGCTA 1800

OY 1801 GCTAGAGTTTATAGGAATGAGTATGCGAGTGAATATGGCATGGCTTTTATTTATGCTAGTT 1860  
 DB 1801 GCTAGAGTTTATAGGAATGAGTATGCGAGTGAATATGGCATGGCTTTTATTTATGCTAGTT 1860

OY 1861 TCTTGGCCAACTCATTGATGTTTGTATAGACATCACACTTTTAACTTTGTTTC 1920





Db 1155 GCAGTTGCAAGAGAGATGAAGTATCTGCAGCTAACCTGCTCTTATAATCAGACACT 1214  
Qy 1257 GAGGTGGAAGTATGAGGGTCCATCTGACTCCTTCAAGGCCCTTGTGATATGCGAGCTGT 1316  
Db 1215 AAGATGGAATACGAGGGCTCCTTCAGATCTTCAAGGCACCTGTTGATGCTGCTGT 1274  
Qy 1317 GCATTCATGCTCCCTCTTTCGATTCACCTTGGCCACAGTGTAGTAGAGAGAAAGAAA 1376  
Db 1275 ACACCTCTTCTCCCTCTCTGATTTCTGCGCCACGAGGTCCGAGAAACAAGAGGGA 1334  
Qy 1377 TAATCAAGCCTTAAGAGACGCTCTTGAAGT---GCACTAGAGGGCCAGAAACCGTATA 1433  
Db 1335 AAGCCCTAATTTCAAGAAACGACCTGCAATGTAGCAGGGAGGATCAGACACACTTTA 1394  
Qy 1434 TCATATCTATGTCAGAGAAAGGGAGGTTTGAGATGGAGTCCATTTACCTGAGGCTAG 1493  
Db 1395 TCATGTTTGTAGAGAAAGAGGGCGGTTTGAATGGAATCAGTCTTTTGTAGGGGTAA 1454  
Qy 1494 CAATTAACCTGGAATGCTGAAGGCTGCTGTTGTTTGAAGTTCACATCCCTGATCT 1553  
Db 1455 AAGTGTGACTCAGGAAGCTCTAGATCTGCAGTCTCGCAAGTCTCAAGTCTTAAACA 1514  
Qy 1554 TGTGCTGTATGGAAGCTGGAAGGCTGGAAGTTTAAAGAGGGGAGTCTTTAAACT 1613  
Db 1515 TGAGGCAGTGTGAGAGAGGAGGCTGGAAGTAAAGGAGACAAAGAGCTTAAAT 1574  
Qy 1614 CTACAAATATACCCANTTGGCTTGACACAGAGACAGCTCTTTATACCTCAGCTTCAA 1673  
Db 1575 ACATGGATTTACCCGCTTGGCCTTAACGCAACGACAGGCTTTGACAACTTCAAAATCGA 1634  
Qy 1674 AGGTGATGCTGATTTGAGAGTCACTTGGAGAACATCCTTTGTGCCAAGTTTGAAGTCA 1733  
Db 1635 GGAATTTGAGTCTAAGTAGTACATTCACATTCAAACAACCTTGTGCTAAATTTGAGGTTG 1694  
Qy 1734 TTTTGTGTAG 1743  
Db 1695 CTTCGCTAG 1704

## RESULT 3

AAF84907  
ID AAF84907 standard; DNA; 2069 BP.

XX AC AAF84907;

XX DT 09-JUL-2001 (first entry)

XX DE Nitrogen-inducible promoter for regulating foreign gene expression.

XX KW nitrogen-inducible promoter; nitrite reductase gene; NIR gene;

XX KW transgenic plant; transgene expression; ss.

XX OS Synthetic.

XX PN WO200125454-A2.

XX PD 12-APR-2001.

XX PF 02-OCT-2000; 2000WO-C011143.

XX PR 04-OCT-1999; 99US-0157133.

XX PA (MEDI-) MEDICAGO INC.

XX PI Vezina L, D'Aoust M;

XX DR WPI; 2001-308228/32.

XX PT Regulating foreign gene transcription in transgenic plants, comprises  
PT transforming a plant (cell) with an expression construct having  
PT nitrogen-inducible promoter, an open reading frame of a gene and a  
PT polyadenylation site

XX PS

Claim 1; Page 30-31; 44pp; English.

XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters  
CC of the nitrite reductase (NIR) gene. The promoter is used for regulating  
CC foreign gene transcription in transgenic organisms. The method uses an  
CC expression construct having a nitrogen-inducible promoter, with(out)  
CC cis-acting sequence, operably linked to the gene to be expressed and  
CC modulated for transcriptional expression of the gene by addition or  
CC removal of a nitrogen inducer, an open reading frame of a gene, and a  
CC 3' polyadenylation signal. The method is useful for regulating the  
CC transcription of transgenes in genetically modified organisms. The  
CC nitrogen-inducible expression cassettes are useful for the controlling  
CC expression of foreign genes in plants.

SQ Sequence 2069 BP; 640 A; 389 C; 335 G; 705 T; 0 other;

Query Match 9.5%; Score 209.4; DB 22; Length 2069;

Best Local Similarity 66.5%; Pred. No. 2.5e-45;

Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy 1486 AGGTCTAGCAATTAACCTGTAAGTCTGTAAGGCTGCTGTTTGAAGTTCACATCC 1545

Db 170 AGATCTAGCAATTAACCTGTAAGTCTGTAAGGCTGCTGTTTGAAGTTCACATCC 229

Qy 1546 CTGAATCTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTATAAGAGGGGAGTGTCT 1605

Db 230 CTGAATCATGTCTGTATGGAAGCCCTGAAAGACCTCAAAATTTCTAAAGGTGGCGATAAA 289

Qy 1606 TTAAGACTCTACAAATATATACCAATTTGGCTTGACACAGACAGCAAGCTCTTTATACCTTC 1665

Db 290 TTGAAGGTTTACAAATATATACCTCGCGGCTTGACACAGAGGCAAGCTCTTTATACCTTC 349

Qy 1666 AGCTTCAAGGATGATGCTGATTTTCAGGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 1725

Db 350 CAGTTCAACGGGATGTTGATTTTCAGAGTCACTTGGAGAACAACTCTTGCCCAAGTTT 409

Qy 1726 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGCTACCTCTGCTCTACCTGAAT 1778

Db 410 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGCTACCTCTGCTCTACCTGAAT 469

Qy 1779 AGCTTCACTTAGCTGAGCATGCTAGAGTTTGTAGGAATGAGTATGGCAGTGAATATGGC 1838

Db 470 AGCTTCTTCACTTAACCTGAGCAATGAAGTTTATAGGAATGAGTATGACCATGGAGTCGCGC 529

Qy 1839 ATGGCTT-----TATTTATGCTAGTCTTCTTGGCAACTCATTTGATGTTT 1884

Db 530 ATGGCTTGTAAAGCTTACCTACTTTGGCCAACTCATCGGGGATTTACATTCAGAAAAT 589

Qy 1885 GTATAAGACATCAGACTTTAAATTTTAAACTTGTCTGTAGAGTGCAGAAATCCATATTTA 1944

Db 590 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGATAAAGTAACTGAATGTTTCATATTTA 649

Qy 1945 ATGCTTAGTTTGTAGTCTTATCTGATCATCT 1977

Db 650 ATGTTGGGTTGTAGTGTTTTACTTGATATAT 682

## RESULT 4

AAF84910

ID AAF84910 standard; DNA; 2124 BP.

XX AC AAF84910;

XX DT 09-JUL-2001 (first entry)

XX DE Nitrogen-inducible promoter for regulating foreign gene expression.

XX KW nitrogen-inducible promoter; nitrite reductase gene; NIR gene;

XX KW transgenic plant; transgene expression; ss.

XX OS Synthetic.

XX



1726	OY	GAAGTCATATTTTCTGTAGCATCGCGTAA-----ATGGTACCTCTGCTCFACCTGCAATT	1778
410	DB	GAGTAATTTTTCTGTAGCATATGTTGAGCTACCTCAATTTACATGATCACCCTAGACAT	469
1779	OY	AGCTTCACCTTAGCTGAGCACTAGCTAGTAGTATTTAGGAATGAGTATGGCAGTGAATATGCG	1838
470	DB	CTCTTTCTTCACTTAAGTATGAGAGAAATGAAGTTTTTAGGAATGAGTATGACCATCGGAGTCGGC	529
1839	OY	ATGCGTT-----TATTTATGCGCTAGTTCTTTGGCCAACTCATTTGATGTGTTTT	1884
530	DB	ATGCGTTTTGTAATGCGCTACCGCTACTTTGGCCAACTCATCGGGGATTTACATTCAGAAAT	589
1885	OY	GTATPAGACATCACACTTTTAATTTTTTAACTTGTTCTGTAGAGAGTGCAATCCCATATTTA	1944
590	DB	ATACATGACTTCAACCATACTTTAAACCCCTTTTTTGAAGATAACTGAATGTTTCATATTTA	649
1945	OY	ATGCTTAGTTTTAGTGCTCTTATCTGATCATCT	1977
650	DB	ATGTTGGGTTGTAGTGTTTTTACTTGATATAT	682

## RESULT 6

AAF84916  
ID AAF84916 standard; DNA: 2232 BP.

09-JUL-2001 (first entry)

**Nitrogen-inducible promoter for regulating foreign gene expression.**

**NW** nitrogen-inducible promoter; **nir** nitrite reductase gene; **NIR** gene;

**KW** transgenic plant; transgene expression; ss.

**Synthetic.**

PN WO200125454-A2.

12-APR-2001.

02-OCT-2000; 2000WO-CA01143.

XX  
PR 04-OCT-1999: 99US-0157133.

XX PA (MEDI-) MEDICAGO INC.

XX  
PI  
vezina L, D'Aoust M:

XX  
DR WPI: 2001-308228/32.

Regulating foreign gene transcription in transgenic plants, comprises transforming a plant (cell) with an expression construct having nitrogen-inducible promoter, an open reading frame of a gene and a polyadenylation site.

PS Claim 1; Page 37-38; 44pp: English.

AA84905-17 represent nitrogen-inducible promoters. They are promoters of the nitrite reductase (NIR) gene. The promoter is used for regulating foreign gene transcription in transgenic organisms. The method uses an expression construct having a nitrogen-inducible promoter, with(out) cis-acting sequence, operably linked to the gene to be expressed and modulated for transcriptional expression of the gene by addition or removal of a nitrogen inducer, an open reading frame of a gene, and a 3' polyadenylation signal. The method is useful for regulating the transcription of transgenes in genetically modified organisms. The nitrogen-inducible expression cassettes are useful for the controlling expression of foreign genes in plants.

Sequence 2232 BP; 686 A; 436 C; 362 G; 748 T; 0 other;

### Query Match

Query Match	9.50;	Score 209.4;	DB 22;	Length 2232;
2232	9.50	209.4	22	2232

Matches	341:	Conservative	0:	Mismatches	151:	Indels	21:	Gaps	2:
QY	1486	AGGTCAGCAATTTAACTCTGAAATGCTGTGAAGCGTCTGCTCTTTTGAAGTTCACATCC	1545						
Db	170	AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGCTTTACGAAGTTCACGTC	229						
QY	1546	CTGAATCTTTGTGCCTGTATGGAAGACTGAAAGGCGCTCAAGCTTATAAGAGGGGGGAGTGC	1605						
Db	230	CTGAATCATGTTCTCTGTATGGAAGCCTGAAAGACCTCAAAATCTTAAAGGTCGCGATAA	289						
QY	1606	TTAAAGACTCTACAAAATATACCCAAATTTGGCTTGACACAGACAGCAACCTCTTTATACCTC	1665						
Db	290	TTGAGGTTTACAAAATATACCTTGGCGGCTTGNACACAGAGCGCAAGCTCTTTATACCTC	349						
QY	1666	AGCTTCAAAGGTGATGCTGATTTTCAGAGATCACTTGGAGAACAAATCCTTTGTGCCAAGTTT	1725						
Db	350	CAGTTTACACGGGGATGTTGATTTTTCAGAAAGTCACTTGGAGAGCAAACTCTTTGTGCCAAGTTT	409						
QY	1726	GAAGTCATTTTGTGTAGCATGCCTAA-----ATGGTACCTCTGCCTACCTCAATTT	1778						
Db	410	GAAGTAATTTTGTGTAGCATATGTTGAGCTACCTTACAATTTACATGATCAGCTAGCATT	469						
QY	1779	AGCTTCTCAGCTAGCTGAGCAGCTAGCTAGAGTATTTTAGGAATGAGTATGGCAGTCAAAATGCG	1838						
Db	470	AGCTCTTTCACCTTAACCTGAGAGAAATGAATTTTAGGAATGAGTATGACCATGGAGTCGCG	529						
QY	1839	ATGGGCTT-----TATTTATGCGTAGTTTCTTGGCCAACTCATTTGATGTTTTT	1884						
Db	530	ATGGCTTTGTAATGCGCTACCCCTACTCTTTGGGCCAACTCATCGGGGATTTTACATTCAGAAAAT	589						
QY	1885	GTATAGACATCACACTTTAAATTTTAAACTTGTGTTCTGTAGAGAGTGCNAATCCATATTTA	1944						
Db	590	ATACATGATCTTCACACATPACTTAAACCCCTTTTGTGAAGATAACTGAATGTTTCATATTTA	649						
QY	1945	ATGCTTAGTTTTAGTGCCTTATCTGATCATCT	1977						
Db	650	ATGTTGGGTTGTAGTGTGTTTTTACTTTGATTTAT	682						

## RESULT 7

RESULT /  
AAF84906  
ID AAF84906 standard; DNA; 2808 BP.

AA  
DT 09-JUL-2001 (flrst entry)

DE Nitrogen-inducible promoter for regulating foreign gene expression.

nitrogen-inducible promoter: nitrite reductase gene: NIR gene:

KW nitrogen-inducible promoter; nitrite reductase

XX Synthetic.

XX PN WO200125454-A2.

12-APR-2001.

XX  
PF 02-OCT-2000: 2000WO-CA01143.XX  
PR 04-OCT-1999: 9911S-0157133XX  
PA (MERT-) MEDTCAGO TNC

XX  
PT  
Vezina I. D'Acoust M:

XX  
WPY: 3001-309338/33

Regulating foreign gene transcription in transgenic plants, comprises transforming a plant (cell) with an expression construct having nitrogen-inducible promoter, an open reading frame of a gene and a polyadenylation site .

### Query Match

Query Match	9.50;	Score 209.4;	DB 22;	Length 2232;
2232	9.50	209.4	22	2232



Claim 1; Page 29-30; 44pp; English.

AA84305-17 represent nitrogen-inducible promoters. They are promoters of the nitrite reductase (NIR) gene. The promoter is used for regulating foreign gene transcription in transgenic organisms. The method uses an expression construct having a nitrogen-inducible promoter, with(out) cis-acting sequence, operably linked to the gene to be expressed and modulated for transcriptional expression of the gene by addition or removal of a nitrogen inducer, an open reading frame of a gene, and a 3' polyadenylation signal. The method is useful for regulating the transcription of transgenes in genetically modified organisms. The nitrogen-inducible expression cassettes are useful for the controlling expression of foreign genes in plants.

Sequence 2808 BP: 879 A; 502 C; 481 G; 946 T; 0 other; xx

Query Match 9.50: Score 209.4: DB 22: Length 2808:

Best Local Similarity 66.50; Pred. No. 2.9e-45;

Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

1486	QY	AGGCTCTAGCAAAATTTACTCTGAATGCTGTGAAGCGCTGCTGTGTGTTTTGAAGTTCACATCC	1545
909	Db	ATCTTTAGCAAAATTTACTCTGAGAGTCTTCAAGACTGCTGTCTTTACGAAGTTTCACGCTC	968
1546	QY	CTGAATCTTGCGCTGTATGGAAGACTGAAAGGCGCTGAAGTTATTAAGAGGGGGAGTGCT	1605
969	Db	CTGAATCATCTTCCCTGTATGGAAGCGTGAAGAGACTCAAAATTTCAAAGGTGGCGATAAA	1028
1606	QY	TTAAACCTCTACAAATATACCCTAATTTGGCTGTACACAGAGACAGCTCTTTATACCTTC	1665
1029	Db	TTGAAGGTTTTACAAATATATACCTCGCGGCTTGTACACAGGACAGCTCTTTATACCTTC	1088
1666	QY	AGCTTCAAAGGTCAGCTGATTTTCAGGAGTCACTTGTGAGACAATCTTGTGCCAAGTTT	1725
1089	Db	CAGTTTCAACGGGATGTTGATTTTCAGAAGTCACTTGTGAGACAATCTTGTGCCAAGTTT	1148
1726	QY	GAAGTCAATTTTTGTGTAGCATGCGCTAA-----ATGCTACCTCTGCTCTACCTGAAAT	1778
1149	Db	GAAGTAATTTTTGTGTAGCATATGTGTGAGCTACCTCAAAATTTACATGATCATCCTAGCAAT	1208
1779	QY	AGCTTTCATTTAGCTGAGCACTAGCTAGAGATTTTGAAGAA'TGAGTATGTGGCAGTGAATATGGC	1838
1209	Db	AGCTCTTTCACTTAACCTGAGAGAA'TGAAGTTT'TAGGAATGACTATGACCATGGAGTCGCG	1268
1839	QY	ATGGCGTT-----TATTTATGCGCTAGTTCTTGTGGCCAAC'TCATTGATGATTTTT	1884
1269	Db	ATGGCTTTGTAATGCCCTACCTTGTGGCCAAC'TATCGGGGATTTTACATTCAGAAAT	1328
1885	QY	GTATAAGACATCACACTTTAATTTTAAACTTGTCTGTGAAGAGTGCAAATCCATATTTA	1944
1329	Db	ATACATGACTTCAACCATACTTTAAACCCCTTTTGTGAAGATAAC'TGAATGTTTCATATTTA	1388

**DECI 7 8**

RESULI D  
AAF84909

ID AAF84909 standard; DNA; 2863 BP.

[illegible]

AC AAF84909;

XX	
DT	Nitrogen-inducible promoter for regulating foreign gene expression.
XX	
XX	
DE	nitrogen-inducible promoter; nitrite reductase gene; NIR gene;
XX	transgenic plant; transgene expression; ss.
KW	
KW	

XX  
XX  
XX

OS Synthetic.

Db 1389 ATGTTGGGTTCTAGTCTTTTACTTGATTAT 1421



Qy	1486	AGGCTCAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTGTTGTTTGAAGTTCACATCC	1545
Db	909	AGATCTAGCAATTTAACTCTGGAGTCTTCAAGACTGCTGTCTTACGAAGTTCACGTCC	968
Qy	1546	CTGAATCTTGTGCCTGTATGGAAGACTGAAAGGCTGAAGTCTATAGAGGGGGAGTGCT	1605
Db	969	CTGAATCATGTTCTGTATGGAAGCTGAAAGACCTCAATTTCTAAAGGTGGCGATAA	1028
Qy	1606	TTAAAACTCTACAAATATACCNAATTGGCTTGACACAGACAGACGCTCTTTATACCTTC	1665
Db	1029	TTGAAGGTTTACAAATATACCCTGGGCGCTTGACACAGAGGACAGCTCTTTATACCTTC	1088
Qy	1666	ACGTTCAAAGGTGATGCTGATTTCAAGGAGTCACCTTGGAGAACAAATCCTTGTGCCAAGTTT	1725
Db	1089	CAGTTTCNAACGGGGATGTGATTTCAAGAACTCACCTTGGAGAGCAATCCTTGTGCCAAGTTT	1148
Qy	1726	GAAGTCATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCCTCTACCTGAAAT	1778
Db	1149	GAAGTAATTTTGTGTAGCATATGTTGAGCTACCTTACAATTTACATGATCACTAGCAAT	1208
Qy	1779	AGCTTTCACCTTACGTGAGCACTACGTAGAGTTTTTTAGGAATGAGTATGGCAGTGAAATGTCG	1838
Db	1209	AGCTCTTTTCACTTAACTGAGAGAATGAAGTTTTAGGAATGAGTATGACCATCGAGTCGCG	1268
Qy	1839	ATGGGCTT-----TATTTATNGCCTACTGTTCTTTGGCCCACTCATTTGATGATGTTTT	1884
Db	1269	ATGGCTTTGTAAAGCCCTACCGCTACTTTGGCCCACTCATCGGGGATTTACCTTCAGAAAT	1328
Qy	1885	GTAATAGACATCACACTTTAAATTTAACTGTGTTCCTGTAGAAGTGCAAAATCCATATTTA	1944
Db	1329	ATACATGACTTTCACCACTACTTTAAACCCCTTTTTTTTGAAGATAACTGAATGTTTCATATTA	1388
Qy	1945	ATGCTTAGTTTTAGTGCTCTTATCTGATCATCT	1977
Db	1389	ATGTTGGGCTGTAGTGTGTTTTTACTTGATTATAT	1421

RESULT 11	
AAF84905	AAF84905 standard; DNA; 3714 BP.
XX	
XX	AAF84905;
XX	
XX	23-JUL-2001 (first entry)
DE	Nitrogen-inducible promoter for regulating foreign gene expression.
DE	
XX	nitrogen-inducible promoter; nitrite reductase gene; N1R gene;
KW	transgenic plant; transgene expression; SS.
KW	
XX	
OS	Synthetic.
XX	
PN	WO200125454-A2.
XX	
PD	12-APR-2001.
XX	
PF	02-OCT-2000; 2000WO-CA01143.
XX	
PR	04-OCT-1999; 99US-0157133.
XX	
PA	(MEDI-) MEDICAGO INC.
XX	
PI	Vezina L, D'Aoust M;
XX	
DR	WPI: 2001-308238/32.
XX	
PT	Regulating foreign gene transcription in transgenic plants, comprises
PT	transforming a plant (cell) with an expression construct having
PT	nitrogen-inducible promoter, an open reading frame of a gene and a
PT	polyadenylation site
XX	
PS	Claim 1; Page 28-29; 44pp; English.



ID ABL76406 standard; cDNA; 287 BP.  
AC ABL76406;  
XX  
XX  
XX 14-MAY-2002 (first entry)  
XX  
DE Corn tassel-derived polynucleotide (cdps) SEQ ID NO:5780.  
XX  
XX Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs;  
KW inheritance; characteristic; growth; development; disease resistance;  
KW environmental adaptability; quality; yield; molecular marker;  
KW multigene trait; plant breeding; corn tassel; gene; ss.  
XX  
XX Zea mays.  
XX  
XX US2001051335-A1.  
XX  
XX 13-DEC-2001.  
XX  
XX 16-APR-1999; 99US-0294093.  
XX  
XX 21-APR-1998; 98US-082567P.  
XX  
XX (LALG/) LALGUDI R V.  
PA (ITOL/) ITO L Y.  
PA (SHER/) SHERMAN B K.  
XX  
XX Lalgudi RV, Ito LY, Sherman BK;  
XX  
XX WPT; 2002-163647/21.  
XX  
XX Novel purified corn tassel-derived polynucleotide useful for  
PT determining altered gene expression, to recover regulatory elements and  
PT to follow inheritance of desirable characteristics through hybrid  
PT breeding programs  
XX  
PS Claim 1: SEQ ID 5780; 201pp; English.  
XX  
XX The present sequence describes a purified corn tassel-derived  
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence  
CC selected from those given in ABL70627 to ABL76833. The cdps sequences  
CC encode corn tassel-derived polypeptides (CDPs). The cdps sequences (1)  
CC can be used for determining altered gene expression, to recover  
CC regulatory elements and to follow inheritance of desirable  
CC characteristics through hybrid breeding programs. (1) are also useful  
CC in the evaluation, and alteration of desired characteristics associated  
CC with growth and development, disease resistance, environmental  
CC adaptability, quality and yield, and as molecular markers for studying  
CC inheritance of multigene traits, in a plant breeding program. (1) can be  
CC used to produce a tassel-specific profile of gene transcription, a  
CC transcript image, to clone regulatory elements for use in transformation  
CC vectors, to express a polypeptide, to identify, isolate or extend  
CC identical or related corn tassel nucleic acid sequences from DNA  
CC libraries, in nucleic acid hybridisation or amplification technologies,  
CC as query sequences to determine homology of known sequences, as probe  
CC for use in Southern or Northern hybridisation, and to identify the  
CC presence of and/or to determine the degree of similarity between two  
CC (or more) nucleic acid sequences.  
XX  
XX  
XX Sequence 287 BP; 78 A; 57 C; 62 G; 90 T; 0 other;  
Query Match 3.8%; Score 84.2; DB 24; Length 287;  
Best Local Similarity 67.2%; Pred. NO. 2.5e-12;  
Matches 119; Conservative 0; Mismatches 58; Indels 0; Caps 0;  
Oy 658 GCATTGGTTACTCAACAGTGGACAGTTCCTCGCATCTCGCATCAATGCAATCAGCA 717  
Db 39 GGACTGGAGTAATGCTACATCTTCTGTAGAGGGTATCTCTCGCATCAATGCAATCATCT 98  
Oy 718 GAATACATCTCTGAGAACATATTTGCGATGGCAAGCAGGGGATACATGTAATG 777  
Db 99 CAATATTATTCAAGAAATAGTATTGCTGGCTCGAGGAGGGGTACAGATTGTGATG 158

Oy 778 ACAACCACTCTATCTTCGGATGTTCCCTGGTGGATATTTTTCATGGCTCAGTATGAT 834  
Db 159 ACAATCAGCCTTTCTTCACACGCTCCAGTTGGCTACTCTTTCATGGCTCAATATGAT 215  
RESULT 15  
AAC40119  
ID AAC40119 standard; DNA; 1461 BP.  
XX  
XX AAC40119;  
AC  
XX  
DT 17-OCT-2000 (first entry)  
XX  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 27123.  
DE  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
XX Arabidopsis thaliana.  
OS  
XX  
XX EP1033405-A2.  
PN  
XX  
XX 06-SEP-2000.  
PD  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PF  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 06-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 16-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 21-APR-1999; 99US-0130077.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 21-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.

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PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 21-JUN-1999; 99US-0139899.
PR 21-JUN-1999; 99US-0140353.
PR 21-JUN-1999; 99US-0140354.
PR 21-JUN-1999; 99US-0140355.
PR 21-JUN-1999; 99US-0140695.
PR 21-JUN-1999; 99US-0140823.
PR 21-JUN-1999; 99US-0140991.
PR 21-JUN-1999; 99US-0141287.
PR 21-JUN-1999; 99US-0141842.
PR 21-JUN-1999; 99US-0142154.
PR 21-JUN-1999; 99US-0142055.
PR 21-JUN-1999; 99US-0142390.
PR 21-JUN-1999; 99US-0142803.
PR 21-JUN-1999; 99US-0142920.
PR 21-JUN-1999; 99US-0142977.
PR 21-JUN-1999; 99US-0143542.
PR 21-JUN-1999; 99US-0143624.
PR 21-JUN-1999; 99US-0144005.
PR 21-JUN-1999; 99US-0144085.
PR 21-JUN-1999; 99US-0144086.
PR 21-JUN-1999; 99US-0144325.
PR 21-JUN-1999; 99US-0144331.
PR 21-JUN-1999; 99US-0144332.
PR 21-JUN-1999; 99US-0144333.
PR 21-JUN-1999; 99US-0144334.
PR 21-JUN-1999; 99US-0144335.
PR 21-JUN-1999; 99US-0144352.
PR 21-JUN-1999; 99US-0144632.
PR 21-JUN-1999; 99US-0144684.
PR 21-JUN-1999; 99US-0144814.
PR 21-JUN-1999; 99US-0145086.
PR 21-JUN-1999; 99US-0145088.
PR 21-JUN-1999; 99US-0145088.
PR 21-JUN-1999; 99US-0145087.
PR 21-JUN-1999; 99US-0145089.
PR 21-JUN-1999; 99US-0145192.
PR 21-JUN-1999; 99US-0145145.
PR 21-JUN-1999; 99US-0145218.
PR 21-JUN-1999; 99US-0145224.
PR 21-JUN-1999; 99US-0145276.
PR 21-JUN-1999; 99US-0145913.
PR 21-JUN-1999; 99US-0145918.
PR 21-JUN-1999; 99US-0145919.
PR 21-JUN-1999; 99US-0145951.
PR 21-JUN-1999; 99US-0146385.
PR 21-JUN-1999; 99US-0146386.
PR 21-JUN-1999; 99US-0146388.
PR 21-JUN-1999; 99US-0146389.
PR 21-JUN-1999; 99US-0147038.
PR 21-JUN-1999; 99US-0147204.
PR 21-JUN-1999; 99US-0147302.
PR 21-JUN-1999; 99US-0147192.
PR 21-JUN-1999; 99US-0147260.
PR 21-JUN-1999; 99US-0147303.
PR 21-JUN-1999; 99US-0147416.
PR 21-JUN-1999; 99US-0147493.
PR 21-JUN-1999; 99US-0147932.
PR 21-JUN-1999; 99US-0148171.
PR 21-JUN-1999; 99US-0148319.
PR 21-JUN-1999; 99US-0148341.
PR 21-JUN-1999; 99US-0148565.
PR 21-JUN-1999; 99US-0148684.

PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0150366.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158569.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.14; Score 50; DB 21; Length 1461;
Best Local Similarity 55.18; Pred. No. 0.0072;
Matches 98; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 981 GAACCGTGATGGAGACTGAACAAAGTGAAGCCCTGAAGCACTACAAATTTAGCTTACG 1040
DB 877 GAAGCAAAATGGTACGATCACCTCCCACTCCCGCTATGTGCACACTACAAATTCGCTTGC 936
QY 1041 GTTTGAAATTCGAATGAGGAAGATTATGTAAGTGAAGCAATTTCCCAATCCCTTTGTC 1100
DB 937 ATCGAANAACACAGCTGTTGAGTCATACGTCACCGAGAGACCTTTCTATGCGCTCGACTC 996
```



GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 01:10:31 ; Search time 2820 Seconds  
(without alignments)  
12623.291 Million cell updates/sec

Title: US-09-913-858A-1  
Perfect score: 2198  
Sequence: 1 actaactcaacgtgcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :			
EST:*			
1:	em_estba:*		
2:	em_esthum:*		
3:	em_estin:*		
4:	em_estm:*		
5:	em_estov:*		
6:	em_estpl:*		
7:	em_estro:*		
8:	em_htc:*		
9:	gb_est1:*		
10:	gb_est2:*		
11:	gb_htc:*		
12:	gb_est3:*		
13:	gb_est4:*		
14:	gb_est5:*		
15:	em_estfun:*		
16:	em_estom:*		
17:	gb_gss:*		
18:	em_gss_hum:*		
19:	em_gss_inv:*		
20:	em_gss_pln:*		
21:	em_gss_vrt:*		
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23:	em_gss_mam:*		
24:	em_gss_mus:*		
25:	em_gss_other:*		
26:	em_gss_pro:*		
27:	em_gss_rod:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	437.6	19.9	532	13	BM143091
2	378.6	17.2	689	13	BM099511
3	337.2	15.3	571	13	BM099511_EBES01_SQ
4	332.2	15.1	517	12	BJ464838
5	280.2	12.7	690	14	BG790911
6	257.8	11.7	701	14	BQ659171

7	248.8	11.3	856	10	BEA12601
8	231.2	10.5	803	12	BF628851
9	223.8	10.2	420	9	AJ475410
10	218.8	10.0	700	9	AL503218
11	212.6	9.7	729	14	BM816799
12	208	9.5	560	14	BM737488
13	195.2	8.9	619	12	BG465531
14	191	8.7	383	13	BM443222
15	189	8.6	321	12	BG263065
16	187.2	8.5	674	13	BJ170811
17	179	8.1	844	12	BF261629
18	172.8	7.9	388	14	BQ463217
19	156.4	7.1	866	17	BH431446
20	156.4	7.1	753	17	BH418424
21	151.8	6.9	735	17	BH423619
22	146	6.6	526	9	AL500587
23	141.8	6.5	669	17	BG7847
24	136.8	6.2	772	17	BH535486
25	134.4	6.1	806	17	BH441710
26	133.8	6.1	269	10	AW695306
27	133.6	6.1	543	17	CNS00W0V
28	131.6	6.0	484	14	BM737489
29	130	5.9	496	10	AW498425
30	127.4	5.8	539	17	BH783802
31	111	5.1	529	14	BQ765453
32	110	5.0	240	9	AJ477062
33	105	4.8	604	17	AQ271924
34	105	4.8	616	17	AQ328306
35	104.6	4.8	344	17	BH440694
36	101.6	4.6	791	10	BE034958
37	101	4.6	472	12	BG241740
38	96.4	4.4	500	14	BM885010
39	89.8	4.1	568	13	BJ201098
40	86.2	3.9	235	14	BQ623003
41	84.6	3.8	433	10	AV792413
42	84.4	3.8	501	13	BI922470
43	78.6	3.6	663	17	AQ158899
44	78.6	3.6	772	17	AQ840447
45	73.8	3.4	568	17	BH776651

ALIGNMENTS

RESULT 1	BM143091	BM143091	532 bp	mRNA	linear	EST 29-NOV-2001
LOCUS	sa339d07.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl066-5150 5' similar to TR:Q9ST51 Q9ST51 FUCT C3 PROTEIN. ;					
DEFINITION	mRNA sequence.					
ACCESSION	BM143091	GI:17153158				
VERSION	EST.					
KEYWORDS	soybean.					
SOURCE	Glycine max					
ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.					
REFERENCE	1 (bases 1 to 532)					
AUTHORS	Shoenaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Person, B., Swaller, T., Gibbons, M., Pope, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, J., Waterston, R. and Wilson, R.					
TITLE	Public Soybean EST Project					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Shoenaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800					







Email: estevan.wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact via email: ccuresgen.com  
 High quality sequence stop: 421.

# FEATURES

1. 517  
 Location/Qualifiers  
 /organism="Glycine max"  
 /cultivar="Williams"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1064-3675"  
 /clone\_lib="Gm-c1064"  
 /tissue\_type="seedling epicotyls"  
 /dev\_stage="2 week old"  
 /lab\_host="DH10B"  
 /note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2:  
 XhoI; The cDNA library was constructed from mRNA isolated  
 from the epicotyls of 2 week old seedling for the cultivar  
 Williams. The seedlings were germinated in a growth  
 chamber, excised above the soil level, and the plants  
 were placed in a 100 ppm solution of auxin for 24 hours  
 prior to harvesting. Complementary DNA was synthesized  
 from mRNA using a primer consisting of a poly(dT)  
 sequence with a XhoI restriction site. EcoRI adapters  
 were ligated to the blunt-ended cDNA fragments followed  
 by XhoI digestion. The cDNA fragments were directionally  
 cloned into the EcoRI-XhoI restriction site of the  
 pBluescript vector. The ligated cDNA fragments were  
 transformed into DH10B host cells (GibcoBRL). This  
 library was constructed in the laboratory of Dr. Randy  
 Shoemaker."

BASE COUNT 147 a 88 c 110 g 172 t  
 ORIGIN  
 Query Match 15.1%; Score 332.2; DB 12; Length 517;  
 Best Local Similarity 83.7%; Pred. No. 1.1e-49;  
 Matches 426; Conservative 0; Mismatches 73; Indels 10; Gaps 4;

Oy 1456 GGAAGGTTTCAGATGAGTCCATTTACCTGAGGCTAGCATTTTAACTCTGATGCTGTG 1515  
 Db 1 GGAAGGTTTCAGATGAGTCCATTTACCTGAGGCTAGCATTTTAACTCTGATGCTGTG 60  
 Oy 1516 AAGGCTCTCTTTTGAAGTTCACATCCCTGAACTTGTGCTGTATGGAAGACTGAA 1575  
 Db 61 AAGTTTCTCTCTTTTGAAGTTCACATCCCTGAACTTGTGCTGTATGGAAGACTGAA 120  
 Oy 1576 AGGCTGAAGTTTAAAGAGGGGGAGTCTTTAAACTCTCAAAATATACCAATGGC 1635  
 Db 121 AGACCTGAATTTCTAGAGGGGCAATGATTTAAACTCTCAAAATATACCAATGGG 180  
 Oy 1636 TTGACACAGACAAGCTCTTTATACCTTCAGCTTCAAGGTGATGCTGATTTCCAGAGT 1695  
 Db 181 TTGACACAAAGACAAGCTCTTTATACCTTCAGCTTCAAGGGGATGAGATTTCCAGAGT 240  
 Oy 1696 CACTTGGAGAACAACTCTTGTGCGCAAGTTTGAAGTCAATTTTGTGATGAGCTGCTAAAT 1755  
 Db 241 CACTTGGAAAGCCATCTTGTGCGCAAGTTTGAAGTCAATTTTGTGATGAGCTGCTAG-T 299  
 Oy 1756 GGTACCTCTGCTTACCTCAATAG--CTTCACTTAGCTGAGCACTAGCTAGAGTTTATG 1813  
 Db 300 GGCTCTCTGCTCTACATGAATAGTCTTCTCACTTAACTGAGC----GGTAGAGTTTATG 355  
 Oy 1814 GAATGATATGGCAGTGAATATGGCATGGCTTTATTTATGCTAGTTTCTTGGCCAACTC 1873  
 Db 356 GGATGAGTATGGCAATGAAACTGGCATGGCTTTATTTATGATAGCTTCTTGACCAACTC 415  
 Oy 1874 ATTGATCTTTTGTATGACATCACTTAAATTTAACTGTTTCTGT---AGAAGTG 1930  
 Db 416 ATTGATGATTTATTTCAAGATCAATCTTACTTTTGAATCTTTTGTGATCAAGAGTG 475  
 Oy 1931 CAATGCATATTTAATGCTTTAGTTTAGT 1959  
 Db 476 AGGTTCCATATTTAATGCTTTAGTTTAGT 504

# RESULT 5

LOCUS B0659171/c

DEFINITION HD01K22W HD Hordeum vulgare cDNA clone HD01K22 3-PRIME, mRNA

ACCESSION B0659171

VERSION B0659171.1

KEYWORDS GI:21800304

SOURCE EST

ORGANISM Hordeum vulgare

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae

; Triticeae; Hordeum.

1 (bases 1 to 690)

Michalek, W., Meschke, W., Pleissner, K.-P. and Graner, A.

EST sequencing and analysis in barley

Unpublished (2000)

JOURNAL Contact: Stein Nils

COMMENT Molecular Markers Group, Department Genbank

Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, 06466, Gatersleben, Germany

Tel: 039482-5522

Fax: 039482-5535

Email: stein@ipk-gatersleben.de

Insert Length: 690 Std Error: 0.00

Plate: 1 row: K column: 22

Seq primer: T7.

Location/Qualifiers

1. 690

/organism="Hordeum vulgare"

/cultivar="Golden Promise"

/db\_xref="GABI:132513"

/db\_xref="taxon:4513"

/clone="HD01K22"

/clone\_lib="HD"

/tissue\_type="callus"

/dev\_stage="callus (5-10 mm in diameter)"

/lab\_host="XL10-Gold"

/note="Vector: pBluescript SK+; Site\_1: EcoRI (5'-end of

cDNA); Site\_2: XhoI (3'-end of cDNA); Due to a cloning

artefact caused by the kit, in most cases the EcoRI site

is NOT present, as well as the EcoRI adapter used for

cloning. To excise the insert, restriction sites upstream

EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also

due to the cloning system used Blue/White selection for

recombinants is not 100% reliable. Average insert size is 1

kb.

BASE COUNT 210 a 142 c 122 g 216 t

ORIGIN

Query Match 12.7%; Score 280.2; DB 14; Length 590;

Best Local Similarity 68.1%; Pred. No. 1.7e-40;

Matches 390; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Oy 1172 ATATTAAAGAGATAGAGGATGTGTGACTGTGTGCGCAAGACCATGAGATATACGAGAA 1231

Db 690 ACATCAAGGAGCTTGATGATGCTATTTTCAGTTGCGAAGACAATGAACATATTCGACAA 631

Oy 1232 ATCCCGAAGCATATATCAATCATTCAGCTGGAAGTATGAGGTCCTCATCTGACTCTTCA 1291

Db 630 ATCTGTATGCTTTTAACTCAATCTTTGAGGTGGAAGTATGATGCTCCATCTGATCTTTCA 571

Oy 1292 AGGCCCTTGTGGATATGGCAGCTGTCATTTATCTGTCGCTCTTTGATTCATCTTGGCCA 1351

Db 570 AGGCACCTTATTTGACATGGCGCGGTTCATTCATCTCTGCGCTTTGTATACATATCGCTA 511

Oy 1352 CAGTGAGTAGAAGAGGAAGAAATAATCAAGCCTTTTAAAGAGAGCTCTTGAAGTGCA 1411

Db 510 CGAAGATTTCATGAAAAAGAAAGAAAAAATCCCAAAATTTATCAATCGCTCGTGTAGTGCT 451

Oy 1412 CTAGAGGCCAGAAACCGGTATATCATATCTATGTCAGAGAAGGGAGGTTTTCAGATGG 1471

Db 450 CCAGCAAGAGGACAGTATACCACTTATTTGTGACAGAGAGGCGGTTTAAACAG 391  
 QY 1472 AGTCCATTACCTGAGGCTAGCAATTAACCTGAAGCTGCTGTTGTTT 1531  
 Db 390 AGACATTTATCTAAGATCAGATGAGTAACTTTAGGAGCTTTGAGTCTGCTGCAGC 331  
 QY 1532 TGAAGTTCACATCCCTGAATCTTGTGCTGTATGGAAGACTGAAGCCCTGAAGTTATAA 1591  
 Db 330 ATAAATTTAGTCTCCCTCAAGCATGCTCTATATGGAAGGATGAAGGCCATCAAGTATTC 271  
 QY 1592 GAGGGGGAGTGTCTTTAAACTCTACAAAATATACCAATTTGCTTGACACAGACAGAAC 1651  
 Db 270 GAGTGGGATGAATGGAAGTGTACAAATTTATCCATAGTCTTTACAGAACGACAAAG 211  
 QY 1652 CTCCTTTACCTTACGCTTCAAGGTCAGCTGATTTTCAGAGTCTACTTGGGAGCAATC 1711  
 Db 210 CATTATATAAATTTCAATTCAGTGCACATGCTGAAGTGTCTAGATATATTAAGGGCCATC 151  
 QY 1712 CTGTGCCAAGTTTGAAGTCAATTTTGTGTAGC 1744  
 Db 150 CATGTGCAAGAGCTTGAGGTGATTTTGTATATAAC 118

RESULT 6  
 BQ167130/c  
 LOCUS  
 DEFINITION  
 WHE0946\_F09\_K18Y Wheat 5-15 DAP spike mRNA linear EST 25-APR-2002  
 aestivum cDNA clone WHE0946\_F09\_K18, mRNA sequence.

ACCESSION  
 BQ167130  
 VERSION  
 BQ167130.1 GI:20311201  
 SOURCE  
 EST.

ORGANISM  
 Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 1 (bases 1 to 701)

REFERENCE  
 AUTHORS  
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.  
 The structure and function of the expressed portion of the wheat  
 genomes - 5-15 DAP spike cDNA library

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105959773  
 Fax: 5105959818  
 Email: oandersn@pw.usda.gov

FEATURES  
 source  
 1..701  
 /organism="Triticum aestivum"  
 /cultivar="Chinese Spring"  
 /db\_xref="taxon:4565"  
 /clone="WHE0946\_F09\_K18"  
 /clone\_11p="wheat 5-15 DAP spike cDNA library"  
 /tissue\_type="Spike"  
 /dev\_stage="Adult plant"  
 /lab\_host="E. coli SOUR"  
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
 Site\_1: EcoRI; Site\_2: XhoI; Plants were grown in the  
 greenhouse. Spikes at 5, 10 and 15 DAP were harvested,  
 total RNA and poly(A) RNA were prepared, a cDNA library  
 was made, and the cDNA clones were in vivo excised to  
 give plus-script phagemids in the TJ Close lab (Choi,  
 Close, Fenton) at the University of California.

BASE COUNT 218 a 153 c 124 g 206 t  
 ORIGIN  
 Query Match 11.7%; Score 257.8; DB 14; Length 701;  
 Best Local Similarity 68.2%; Pred. No. 1.7e-36;  
 Matches 358; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 1220 ATCTACAGAAATCCCGAGCATATACTCAATTCAGCTGGAAGTATGAGGTCAT 1379  
 Db 701 ATATTGCTGCAATCTGATGCTTTTATCAATCTTGAGGTGAAGTACCATGCTCAT 642  
 QY 1280 CTGACTCTCTCAAGGCCCTTGTGGATATGGCAGCTGTGCATTCATCGCGCTTTTSCA 1339  
 Db 641 CTGATTCTTTCAAGGCACTTATTGACATGGCAGCGTTTCAATTCATCTCTGCGCTTTGCA 582  
 QY 1340 TTCACTTGGCCACAGTGTAGTAGAGAGAGAAATAATCAAGCTTAAAGAGAGCTC 1399  
 Db 581 TACATATCGCTACGAAGATTTCAGAAAGAGAGAAAGCCCAAAATTTATGAATCGCT 522  
 QY 1400 CTTGCAAGTGCCTAGAGGCCAGCAACCGTATATCATATCTATGTCAGAGAAAGGGAA 1459  
 Db 521 CATGTAGTGTCTCCAGCAAGAGGAGCAAGTATACCACTTATTTGTGACAGAGAGAGGGC 462  
 QY 1460 GGTGTGAGATGAGTCCATTTACCTGAGTCTTAGCAATTTAACTCTGAATGCTGTGAAGG 1519  
 Db 461 GGTTTAAGACAGAGAGCAATTTATCTAAGATCAGATCACTTAACTTTAGGAGCTTTGGAGT 402  
 QY 1520 CTGCTGTCTTTTGAAGTTCACTCCCTCACTGTGCTGCTGCTGATGGAAGCTGAAGGC 1579  
 Db 401 CTGCGTGCATGTTAATTTAGTATCCCTCAAGCATGTTCTCTGTATGGAAGATGAAGGC 342  
 QY 1580 CTGAAGTTATAGAGGGGGAGTGTCTTTAAACTCTACAAAATATACCAATTTGGCTTGA 1639  
 Db 341 CATCAAGTATTCGAGCGGGGATGAGTTGAAGGTGTACAAAATTTTACCAATAGGCTTTA 282  
 QY 1640 CACAGAGACAAAGCTCTTTTACCTCAGCTTCAAAAGGTGATGCTGATTTCAGAGAGTCACT 1699  
 Db 281 CAGAGACAAAGCGTTATATAAATTTCAATTCAGTGTAGTCTGAAGTGTCTAGATATA 222  
 QY 1700 TGGAGAACATCTTGTGCCAAGTTTGAAGTCATTTTGTGTAGC 1744  
 Db 221 TTAAGGCCATCATCTGCAAGAGCTTGAGGTGATTTTGTATATAAC 177

RESULT 7  
 BQ12601  
 LOCUS  
 DEFINITION  
 MCG002\_B07B990625 ITEC MCG Barley Leaf/Culm Library Hordeum vulgare  
 cDNA clone MCG002.B07, mRNA sequence.

ACCESSION  
 BQ12601  
 VERSION  
 BQ12601.1 GI:9410447  
 KEYWORDS  
 EST.

SOURCE  
 Hordeum vulgare  
 ORGANISM  
 Hordeum vulgare

REFERENCE  
 AUTHORS  
 Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.  
 International Triticeae EST Cooperative (ITEC): Production of  
 Expressed Sequence Tags for Species of the Triticeae  
 Unpublished (2000)

JOURNAL  
 COMMENT  
 Contact: Graner A  
 Corrensstr. 3, D-06466 Gatersleben GERMANY

Tel: 49 39482 5521  
 Fax: 49 39482 5137  
 Email: a\_granerie@k-gatersleben.de  
 International Triticeae EST Cooperative (ITEC)  
 http://wheat.pw.usda.gov/genome.

FEATURES  
 source 1..856  
 Location/Qualifiers  
 /organism="Hordeum vulgare"  
 /db\_xref="taxon:4513"  
 /clone="MCG002.B07"  
 /clone\_lib="ITEC MCG Barley Leaf/Culm Library"  
 /tissue\_type="leaf/culm"  
 /dev\_stage="etiolated"

BASE COUNT 194 a 211 c 235 g 214 t 2 others

ORIGIN

Query Match 11.3%; Score 248.8; DB 10; Length 856;  
 Best Local Similarity 61.2%; Pred No. 6.1e-35;  
 Matches 498; Conservative 0; Mismatches 289; Indels 25; Gaps 5;

Qy 269 GCTTACCCTGTTGGCTCCGGAGGCAACCCAAAGAGAAATGGAGCAATCTAATGCTC 328  
 Db 67 GCTCCCACTCGCTGACCCAGGGGCAAGCCGCTCGCGCGCTGCGGTGCTCCCGC 126  
 Qy 329 TTGTTGTTGCTTGTGCTCATCGGAGATCGCTTCTGCTAGGTGCTATATGCGCA 388  
 Db 127 TTGCTGTTGCTGTTGCTTCTCGCGAGATCGCTTCTCGCTCGCATGCTGA 186  
 Qy 389 AATACCGCCGATGTTGACTCCCTCGCTGACTTCTTCTACGCTCTCGAGCGGTGCT 448  
 Db 187 AGAAGCTGCGGGGCTGAGAGCGAGCTGACCACTCTCTCCACCGCTCTCTCAACCTGGG 246  
 Qy 449 AAGTGACGATTTGGGTTGGTGTGCTTCTGATCGGAATTCGAATCGTATAGTT 508  
 Db 247 GCGCGGATGC-----GCCCTCGGTAGCGGGGACGACGACGACGAGAGT 288  
 Qy 509 GTGAGGAATGGTGGAGAGGAGGATGCTGCACGATATTCAGGGGCTTTTCCAAAGAGC 568  
 Db 289 GCGAGGAGCGCTTGAGAGGAGGACGCGCTGCTTACGACCGGATTTGAAAGGCTC 348  
 Qy 569 CTATTTTGTCTGAGCTGATCAGGAGTGAAGCTGCTGTGCTGGTGGATGTAATTTG 628  
 Db 349 CTGTACTTGTGCGCGTGTCTTAAGGATTTGGAATAGATGCTCTGTAGGATGTAATTTG 408  
 Qy 629 GGTTTAGTGGGATAGAAAGCCAGATGCGCGATTTGGGTTACCTCAACCAAGTGAACAG 688  
 Db 409 GGTTCAGCTAGTAAGACGCTGATGCTACTTTCCGGAATCGCTCCAGATCCTTCGCTAG 468  
 Qy 689 CTAGCATTCGCTCAATGGAATCAGCAGATATCTATCTGAGACAAATATTCCTCATGG 748  
 Db 469 AGATATCTCAGATCAATGGAATCTCTCAATATTTATTCGAGAACAAATTAATCGGG 528  
 Qy 749 CAAGACGGAGGATATAACATCGTAATGACAAACAGTCTATCTTCGGATGTTCCCTGTT 808  
 Db 529 CTCGAGGAAGAGGTACCAAAATTTGATGACAAACAGGCTTCTCTCAGATGTGCGAGTTG 588  
 Qy 809 GATATTTTTCATGGCTGAGTATGATATGATGACACAGTGCAGCCGACCAAACTGAAGCTG 868  
 Db 589 GCTACTTTTCATGGCTGATATGATATGATATGATGATGATGATGATGATGATGATGATG 648  
 Qy 869 CTCTTCAGCTGCTTTCATTTCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 926  
 Db 649 CCCTAGCTGAGCTTATTTTCCAACTGCGGTGACGAAACTTCCCGTTTTCGCAAGCCCTT 708  
 Qy 927 TGAGGCGCTTGAATAATCAAA--CATCAAAATTTGATCTTATGCT-GCTTGTCCACAGAA 983  
 Db 709 TGACATCTTGAAGCTTAGATGTAATAAATTTGATCTTATGCTAGCTGCTATCGTAA 768  
 Qy 984 CCGTGATGAGAGTGAACAAAGTGGAGCCCTGAGCACTACAAATTTAGCTTAGCTT 1043  
 Db 769 TCGTATGCGAAAGTGGCAAGTGGAA--CTCTAAGGGCTCAATNCAGCTTGTCTTT 826  
 Qy 1044 TGAATTTCAATGAGAAAGATTTATGTAAC 1073

Db 827 TCAGAAATCTAATGAGGANGATTATGTTAC 856

RESULT 8  
 LOCUS BF626851  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

BF626851 803 bp mRNA linear EST 22-OCT-2001  
 HVSME0001105f Hordeum vulgare seedling shoot EST library  
 HVCNDA0002 (Dehydration stress) Hordeum vulgare cDNA clone  
 HVSME0001105f, mRNA sequence.

BF626851  
 BF626851.2 GI:13088342  
 EST

Hordeum vulgare  
 Hordeum vulgare

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
 ; Triticeae; Hordeum.

1 (bases 1 to 803)  
 Wing, R., Close, T.J., Kleinohs, A., Wise, R., Begum, D., Frisch, D., Yu  
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton  
 , R.D., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource  
 for barley genomics: Morex drought-stressed seedling shoot cDNA  
 library

Unpublished (2001)

On Dec 19, 2000 this sequence version replaced gi:11891009.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 478

Seq primer: AATTAACCTCTACTAAAGG

High quality sequence stop: 590.

FEATURES  
 source

1..803

Location/Qualifiers

/organism="Hordeum vulgare"

/cultivar="Morex"

/db\_xref="taxon:4513"

/clone="HVSME0001105f"

/clone\_lib="Hordeum vulgare seedling shoot EST library"

/HVCNDA0002 (Dehydration stress)"

/tissue\_type="Seedling shoot"

/lab\_host="TJC121"

/note="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI;

Seeds were surface sterilized then germinated under axenic  
 conditions in the dark at room temperature on filter paper  
 with water, nystatin and cefotaxime in covered

crystallization dishes. Five-day old seedlings were  
 incubated at 90% RH for 24 hr. Shoots were then harvested,

total RNA was prepared, poly(A) RNA was purified, one  
 primary untemplated cDNA library was made, 600000 pfu were

in vivo excised to give pBluescript SK(-) cDNA phagemids.  
 These steps were performed in the TJ Close laboratory at

the University of California, Riverside (Choi, Close,  
 Fenton). Phagemids were plated and picked at the Clemson

University Genomics Institute (CUGI) (Begum, Palmer,  
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

sequencing and sequence analysis were performed at CUGI  
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).

The sequence has been trimmed to remove vector sequence  
 and contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and  
 sequence analysis see

http://www.genome.clemson.edu/projects/barley. To order

this clone see http://www.genome.clemson.edu/orders Also

see Close TJ, Wing R, Kleinohs A, Wise R (2001)

Genetically and physically anchored EST resources for

barley genomics. Barley Genetics Newsletter 31:29-30.

(http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)\*

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BASE COUNT      166 a      198 c      228 g      211 t
ORIGIN
Query Match      10.5%; Score 231.2; DB 12; Length 803;
Best Local Similarity 58.5%; Pred. No. 8.8e-32;
Matches 470; Conservative 0; Mismatches 313; Indels 21; Gaps 3:
QY 269 GCTTACCCTTTTGGCTCGCGGAGGCAACCCAAAGAGAAATGAGCAATCTAATGCCCTC 328
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Db 1 GCTCCACCTCGCTGACCCAGGCGCAAGCGCTCGCGCGCTCGCGGCTGCTGCCCGC 60
QY 329 TTGTTGTTGCCCTTGTGTCATCGCGGAGATCGGTTTCTCGGTAGGTGGATATGCCCA 388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TTGCTGTTGCTGCTTTTCTCGCGAGATCGGTTCTCTCGGTGCTCGCATGTCGA 120
QY 389 AAAGCCGCCCATCTGACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
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Db 121 AGAACCTCAGCGGCTGAGAGCTGAGACCTGCTCTCCACCGCTCTCTTCAACCTGGG 180
QY 449 AAGGTGACGATTTGGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGG 508
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Db 181 GCGCGCATGC-----GCTCGGGTAGCGGGGACGACGACGACGAGT 222
QY 509 GTGAGCAATGGTTGAGAGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
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Db 223 GCAGAGCGGCTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 282
QY 569 CTATTTTGTGTTGAGCTGATCAGGAGTGGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 628
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Db 283 CTGACTTCTGCGCGCTGCTGCTAAGGATTTGGAATAGATGTTCTGTAGGATGGAATTTG 342
QY 629 GGTGTTAGTGGGATAGAAAGCCAGATGCGCATTTGGTTTACCTCAACCAAGTGGACAG 688
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Db 343 GGTTCACGCTAGTAAGACGCTGATGCTACTTTCGGAATCGCTCCAGATCTTCGTAG 402
QY 589 CTAGCATTTGCGATCAATGGAATCAGCAGATATGCTATGCTGAGAACAAATATGCCATG 748
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Db 403 AGATATCTTCAGATCAATGGAATCGTCTCAATATATTCGGAACAAATATTAATGCGG 462
QY 749 CAAGCGGAGGGATATACATCGTAATGACAACAGTCTATCTTCGGATGTTCTCTGTTG 808
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Db 463 CTCGAGGAAGAGGGTACCAAAATGTGTATGACAACAGGCTTTCTCATATGTCGAGTTG 522
QY 809 GATATTTTTCATGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
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QY 929 AGGCCCTTGAAAATCAAAACATCAAAATG--ATTCTTATGTTGTTGTCACAGGAACCG 986
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QY 987 TGATGGAAGATGACAAAGTGGAGCCCTGAGCACTACAAATTTAGCTTAGCGTTTGA 1046
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QY 1047 AAATTCGAATGAGGAATATGT 1070
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Db 762 GAATTTTATGCGGGATTTTGT 785

RESULT 9
AJ475410
LOCUS      AJ475410
DEFINITION AJ475410 S00008 Hordeum vulgare cdna clone S0000800035C08F1, mRNA
sequence.
ACCESSION  AJ475410
VERSION     AJ475410.1
KEYWORDS    EST.
SOURCE      Hordeum vulgare.

ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 420)
AUTHORS   Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H.
TITLE     Barley EST's
JOURNAL   Unpublished (2002)
COMMENT   Institute of Biotechnology
Contact: Schulman AH
University of Helsinki
P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
Finland. Location/Qualifiers
source     1..420
            /organism="Hordeum vulgare"
            /db_xref="taxon:4513"
            /clone="S0000800035C08F1"
            /clone_lib="S00008"
            /tissue_type="Callus"
            /note="Callus K19"
BASE COUNT      106 a      90 c      101 g      123 t
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Query Match      10.2%; Score 223.8; DB 9; Length 420;
Best Local Similarity 70.9%; Pred. No. 2.7e-30;
Matches 297; Conservative 0; Mismatches 122; Indels 0; Gaps 0:
QY 568 CCTATTTTGTGCTGAGCTGATCAGGAGTGGAACTGCTGTTGGTTGGATGTAATTT 627
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Db 2 CCTGACTTGTGCGCGTCTGCTGAAGGATGGAAATAGATGTTCTGTAGGATGTAATTT 61
QY 628 GGGTTAGTGGGATAGAAAGCCAGATGCGCATTTGGTTACCTCAACCAAGTGGAAACA 687
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Db 62 GGGTTCCAGCTAGAGACGCTGATGCTACTTTCGGAATCGCTCCAGATCTCTCCGTA 121
QY 688 GCTAGCATTTCCGATCAATGGAATCAGCAGATATCTATGCTGAGAACAAATATGCCCATG 747
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Db 122 GAGAGTATCTTCAGATCAATGGAATGCTCTCAATATATATTCGAGAACAAATATTAATCG 181
QY 748 GCAAGCGGAGGGATATAACATCGTAATGACAACAGTCTATCTTCGGATGTTCTGCTGTT 807
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Db 182 GCTCGAGGAAGGGTACCAAAATGTGTATGACAACAGGCTTTCTCTCAGATGTCGAGTT 241
QY 808 GGATATTTTTCATCGGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 867
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Db 242 GGTACTTTTCATGGGCTGAATATGATATCATGTCACCTGTCGCTCCAAAGACTGAAGAG 301
QY 868 GCTCTGACGCTGCTTTTCATTTCCAAATTTGGTGTGCTGCAAAATTTCCGGTTGCAAGCTTT 927
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 GCGCTAGCTGACGCTTTTATTTCCAACTGCGGTGACAGAACTTCGTTTGCAGGCCCTT 361
QY 928 GAGGCCCTTGAAAATCAAAACATCAAAATGATCTTATGTTGGTTGTCACAGGAACCG 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 GAGATGCTTGAAGCTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420

RESULT 10
AL503218
LOCUS      AL503218
DEFINITION AL503218 Hordeum vulgare Barke roots Hordeum vulgare cdna clone
HW01C14T 5', mRNA sequence.
ACCESSION  AL503218
VERSION     AL503218.1
KEYWORDS    GI:12029433
SOURCE      Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 700)
AUTHORS   Michalek,W., Weschke,W., Pleisner,K.-P. and Graner,A.
TITLE     EST sequencing and analysis in barley
```

**JOURNAL  
COMMENT**

Unpublished (2000)  
Contact: Michalek W  
Institute for Plant Genetics and Crop Plant Research  
Corrensstr.3, D-06466 Gatersleben, Germany  
Email: [michalek@ipk-gatersleben.de](mailto:michalek@ipk-gatersleben.de), <http://pgrc.ipk-gatersleben.de>  
Seq primer: T3 primer for 5'end.

## FEATURES

```

/organism="Hordeum vulgare"
/submitter="Baxen"
/db_xref="taxon:4513"
/clone="HM01C147"
/clone_lib="Hordeum vulgare Barke roots"
/tissue_type="roots"
/lab_host="XL0LR"
/notes="vector: plasmid pBK-CMV; Site_1: ECORI; Site_2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature. Cloning
sites: ECORI (5'-end of cDNA) and XhoI (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the kit, in most
cases the ECORI site is NOT present, as well as the ECORI
adapter. Average insert size is 1 kb. Sequence trimming:
Vector sequences and sequence ends were trimmed from the
5'- and 3'-end until a 50 bp window contains less than two
ambiguities. The maximum length was set to 700 bp."
146 a 189 c 199 g 166 t

```

[illegible]

RESULT 11	DEFINITION
BM816799	
LOCUS	

	729 bp	mRNA	linear	EST 05-MAR-2002
BM816799				
HB03F12_T3.ab1	HB Hordeum vulgare cDNA clone HB03F12_T3.ab1 similar to (AC011807)			
		Putative fucosyltransferase [Arabidopsis thaliana], fuc t3 protein [Vigna radiata], fucosyltransferase 3 [Fuct c3] (Arabidopsis thaliana) g113994831emb CAC38048.1 (A404860)		
		alpha1,3-fucosyltransferase [Arabidopsis thaliana], mRNA		

BASE COUNT	moist paper (75% rel. humidity) in light	others
156 a	188 c	204 g
156 b	188 c	178 t
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156 e	188 c	178 t
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156 h	188 c	178 t
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156 k	188 c	178 t
156 l	188 c	178 t
156 m	188 c	178 t
156 n	188 c	178 t
156 o	188 c	178 t
156 p	188 c	178 t
156 q	188 c	178 t
156 r	188 c	178 t
156 s	188 c	178 t
156 t	188 c	178 t
156 u	188 c	178 t
156 v	188 c	178 t
156 w	188 c	178 t
156 x	188 c	178 t
156 y	188 c	178 t
156 z	188 c	178 t
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156 ab	188 c	178 t
156 ac	188 c	178 t
156 ad	188 c	178 t
156 ae	188 c	178 t
156 af	188 c	178 t
156 ag	188 c	178 t
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156 aj	188 c	178 t
156 ak	188 c	178 t
156 al	188 c	178 t
156 am	188 c	178 t
156 an	188 c	178 t
156 ao	188 c	178 t
156 ap	188 c	178 t
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156 cn	188 c	178 t
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156 cy	188 c	178 t
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156 da	188 c	178 t
156 db	188 c	178 t
156 dc	188 c	178 t
156 dd	188 c	178 t
156 de	188 c	178 t









GenCore version 5.1.4-p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 01:12:16 ; Search time 117 Seconds  
(without alignments)  
5761.329 Million cell updates/sec

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Perfect score: 2198  
Sequence: 1 actaactcaacgtgctgatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/ins/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ins/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ins/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209.4	9.5	2069	4	US-09-678-300-3
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3	209.4	9.5	2165	4	US-09-678-300-9
4	209.4	9.5	2232	4	US-09-678-300-12
5	209.4	9.5	2808	4	US-09-678-300-2
6	209.4	9.5	2863	4	US-09-678-300-5
7	209.4	9.5	2904	4	US-09-678-300-8
8	209.4	9.5	2971	4	US-09-678-300-11
9	209.4	9.5	3714	4	US-09-678-300-1
10	44.4	2.0	1639	2	US-08-737-5248-1
11	42.4	1.9	662	4	US-08-998-416-185
12	42.4	1.9	665	4	US-08-998-416-937
13	42.4	1.9	701	4	US-08-998-416-701
14	42.4	1.9	711	4	US-08-998-416-786
15	42.4	1.9	724	4	US-08-998-416-683
16	42.4	1.9	828	4	US-08-998-416-1036
17	42.4	1.9	834	4	US-08-998-416-538
18	42.4	1.9	834	4	US-08-998-416-305
19	42.4	1.9	663	4	US-08-998-416-191
20	42.4	1.9	860	4	US-08-998-416-287
21	40.6	1.8	7218	1	US-08-212-463-14
22	40.4	1.8	854	4	US-08-998-416-534
23	39.4	1.8	3573	4	US-08-353-585-4
24	38.6	1.8	6124	4	US-08-213-419B-3
25	38.2	1.7	7218	1	US-08-212-463-14
26	38	1.7	1454	1	US-08-220-958-3
27	37.8	1.7	723	2	US-08-618-911-1

28	37.8	1.7	767	4	US-08-998-416-472	Sequence 472, App
29	37.8	1.7	827	4	US-08-998-416-535	Sequence 535, App
30	37.8	1.7	1578	4	US-09-416-050A-1	Sequence 1, Appl
31	37.8	1.7	1578	4	US-09-664-800-1	Sequence 1, Appl
32	37.8	1.7	1578	4	US-09-663-309-1	Sequence 1, Appl
33	37.8	1.7	1578	4	US-09-661-569-1	Sequence 1, Appl
34	37.8	1.7	4673	1	US-07-638-431-1	Sequence 1, Appl
35	37.8	1.7	4673	5	PCT-US92-00018-1	Sequence 1, Appl
36	37.6	1.7	1371	2	US-08-428-713-1	Sequence 1, Appl
37	37.6	1.7	1371	3	US-08-904-179-1	Sequence 1, Appl
38	37.4	1.7	87350	3	US-08-781-891-79	Sequence 79, Appl
39	37.4	1.7	87543	4	US-09-791-211-3	Sequence 3, Appl
40	37.2	1.7	629	4	US-09-385-982-389	Sequence 389, App
41	36.8	1.7	1058	4	US-09-452-239-11	Sequence 11, Appl
42	36.8	1.7	1353	4	US-09-390-131-1	Sequence 1, Appl
43	36.2	1.6	2073	4	US-09-173-300-3	Sequence 3, Appl
44	36	1.6	2002	4	US-09-819-993-1	Sequence 1, Appl
45	35.8	1.6	1026	4	US-09-116-498-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-678-300-3  
: Sequence 3, Application US/09678300  
: Patent No. 6420548  
: GENERAL INFORMATION:  
: APPLICANT: VOZINA, Louis-Philippe  
: APPLICANT: D'Aoust, Marc-Andr,  
: APPLICANT: MEDICAGO INC.  
: TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF  
: FILE REFERENCE: FOREIGN GENES  
: FILE REFERENCE: 14149-3.PCT\*  
: CURRENT APPLICATION NUMBER: US/09/678,300  
: PRIOR FILING DATE: 2000-10-03  
: PRIOR APPLICATION NUMBER: US 60/157,133  
: NUMBER OF SEQ ID NOS: 32  
: SOFTWARE: FastSeq for Windows Version 3.0  
: SEQ ID NO 3  
: LENGTH: 2069  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: Sequences to be used as promoter for regulating  
: OTHER INFORMATION: expression of foreign genes  
US-09-678-300-3

Query Match 9.5%; Score 209.4; DB 4; Length 2069;  
Best Local Similarity 66.5%; Pred. No. 2.9e-51;  
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy	1486	AGCTCTAGCAATTTAACTCTGAATCTGCTGAAGGCTGCTGTTTGAAGTTCACATCC	1545
Db	170	AGATCTAGCAATTTAACTCTGAAGTCTTCAAGACTGCTGTTTACGAAGTTCACGCTC	229
Qy	1546	CTGAATCTTCTGCTGTATGGAAGACTGAAAGGCTGAAGTTATAAGAGGGGGAGTCT	1605
Db	230	CTGAATCATGTTCTGCTATGGAAGCTGAAAGACCTCAAAATCTAAAAGGTGGCGATAA	289
Qy	1606	TTAAACTCTACAAAATATACCAATTTGGCTTGACACAGACAGCAAGCTCTTTTATACCTTC	1665
Db	290	TTGAAGTCTTACAANAATATACCTCGGGCTTGACACAGAGGCAAGCTCTTTATACCTTC	349
Qy	1666	AGCTTCAAGCTGATCTGATTTTCAGGAGTCACTTTGGAGAGCAATCTTTGTGCCAAGTTT	1725
Db	350	CAGTTCACGGGAGTGTGATTTTCAGAAGTCACTTTGGAGAGCAATCTTTGTGCCAAGTTT	409
Qy	1726	GAAGTCAATTTTCTGTAGCATGCGCTAA-----ATGCTACCTCTGCTCTACCTGAATT	1778
Db	410	GAAGTAATTTTCTGTAGCATATGTTGAGTACCTACAAATTTACATGATCATCAGCATTT	469

QY 1779 AGCTTCACTAGTGCACACTAGTCTAGAGTATTTAGGAATAGTATGCGAGTGAATATGGC 1838  
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QY 1839 ATGCGTT-----TATTATGCTAGTCTTCTGGCCAACCTATTGATGTTT 1884  
DB 530 ATGCGTTTGAATGCGCTACCTACTTTGGCCAACCTATCGGGGATTTACATTCAGAAAT 589  
QY 1885 GTATAGACATCACACTTTAACTTTTAACTTGTCTGTAGAGTGAATATCCATATTTA 1944  
DB 590 ATACATGACTTCAACCATATTAACCCCTTTTGTGAAGTAACTGAATGTTTCATATTTA 649  
QY 1945 ATGCTTATTTAGTGTCTTATCTGATCATCT 1977  
DB 650 ATGTTGGTGTAGTGTGTTTACTTGAATAT 682

## RESULT 2

US-09-678-300-6

: Sequence 6, Application US/09678300

: Patent No. 6420548

: GENERAL INFORMATION:

: APPLICANT: VOZINA, Louis-Philippe

: APPLICANT: D'Aoust, Marc-Andr.

: APPLICANT: MEDICAGO INC.

: TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF

: FILE REFERENCE: 14149-3\*PCT\*

: CURRENT APPLICATION NUMBER: US/09/678,300

: PRIOR FILING DATE: 2000-10-03

: PRIOR FILING DATE: 1999-10-04

: NUMBER OF SEQ ID NOS: 32

: SOFTWARE: FastSeq for Windows Version 3.0

: SEQ ID NO 6

: LENGTH: 2124

: TYPE: DNA

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: Sequences to be used as promoter for regulating

: OTHER INFORMATION: expression of foreign genes

US-09-678-300-6

Query Match 9.5%; Score 209.4; DB 4; Length 2124;  
Best Local Similarity 66.5%; Pred. No. 2.9e-51;  
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTTGAAGTTCACATCC 1545  
DB 170 AGATCTAGCAATTTAACTCTGAAGTCTGCTTCAAGACTGCTGTTTACGAAGTTCACGTC 229  
QY 1546 CTGAATCTTGTGCTGTATGGAAGACTGAAAGGCTGAAGTTATAAGAGGGGGAGTGCT 1605  
DB 230 CTGAATCATGCTTCTGTATGGAAGCTGAAAGACCTCAAACTCTAAAGGTGGCGATAAA 289  
QY 1606 TTAAGCTCTACAAATATATACCAATTTGCTTGACACAGAGCAAGCTCTTTATACCTTC 1565  
DB 290 TTGAAGCTTTACAAATATATACCTTGGCGCTTGACACAGAGCAAGCTCTTTATACCTTC 349  
QY 1666 AGCTTCAAGGCTGATGCTGATTTTCAAGAGTCACTTTGGAGAACAACTCTTGTGCCAAGTTT 1725  
DB 350 CAGTTTCAACGGGATGTTGATTTTCAAGAGTCACTTTGGAGAACAACTCTTGTGCCAAGTTT 409  
QY 1726 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778  
DB 410 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 469  
QY 1779 AGCTTCACTAGTGCACACTAGTCTAGAGTATTTAGGAATAGTATGCGAGTGAATATGGC 1838  
DB 470 AGCTTTTCACTTAACTAGAGAAATGAAGTCTTTAGGAATAGTATGCGAGTGGC 529  
QY 1839 ATGCGTT-----TATTATGCTAGTCTTCTGGCCAACCTATTGATGTTT 1884

DB 530 ATGCGTTTGAATGCTTACCTACTTTGGCCAACCTATCGGGGATTTACATTCAGAAAT 589  
QY 1885 GTATAGACATCACACTTTAACTTTTAACTTGTCTGTAGAGTGAATATCCATATTTA 1944  
DB 590 ATACATGACTTCAACCATATTAACCCCTTTTGTGAAGTAACTGAATGTTTCATATTTA 649  
QY 1945 ATGCTTATTTAGTGTCTTATCTGATCATCT 1977  
DB 650 ATGTTGGTGTAGTGTGTTTACTTGAATAT 682

## RESULT 3

US-09-678-300-9

: Sequence 9, Application US/09678300

: Patent No. 6420548

: GENERAL INFORMATION:

: APPLICANT: VOZINA, Louis-Philippe

: APPLICANT: D'Aoust, Marc-Andr.

: APPLICANT: MEDICAGO INC.

: TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF

: FILE REFERENCE: 14149-3\*PCT\*

: CURRENT APPLICATION NUMBER: US/09/678,300

: PRIOR FILING DATE: 2000-10-03

: PRIOR FILING DATE: 1999-10-04

: NUMBER OF SEQ ID NOS: 32

: SOFTWARE: FastSeq for Windows Version 3.0

: SEQ ID NO 9

: LENGTH: 2165

: TYPE: DNA

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: Sequences to be used as promoter for regulating

: OTHER INFORMATION: expression of foreign genes

US-09-678-300-9

Query Match 9.5%; Score 209.4; DB 4; Length 2165;  
Best Local Similarity 66.5%; Pred. No. 2.9e-51;  
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGTCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTTGAAGTTCACATCC 1545  
DB 170 AGATCTAGCAATTTAACTCTGGAAGTCTTCAAGACTGCTGTTTACGAAGTTCACGTC 229  
QY 1546 CTGAATCTTGTGCTGTATGGAAGACTGAAAGGCTGAAGTTATAAGAGGGGGAGTGCT 1605  
DB 230 CTGAATCATGCTTCTGTATGGAAGCTGAAAGACCTCAAACTCTAAAGGTGGCGATAAA 289  
QY 1606 TTAAGCTCTACAAATATATACCAATTTGCTTGACACAGAGCAAGCTCTTTATACCTTC 1665  
DB 290 TTGAAGCTTTACAAATATATACCTTGGCGCTTGACACAGAGCAAGCTCTTTATACCTTC 349  
QY 1666 AGCTTCAAGGCTGATGCTGATTTTCAAGAGTCACTTTGGAGAACAACTCTTGTGCCAAGTTT 1725  
DB 350 CAGTTTCAACGGGATGTTGATTTTCAAGAGTCACTTTGGAGAACAACTCTTGTGCCAAGTTT 409  
QY 1726 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778  
DB 410 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 469  
QY 1779 AGCTTCACTAGTGCACACTAGTCTAGAGTATTTAGGAATAGTATGCGAGTGAATATGGC 1838  
DB 470 AGCTTTTCACTTAACTAGAGAAATGAAGTCTTTAGGAATAGTATGCGAGTGGC 529  
QY 1839 ATGCGTT-----TATTATGCTAGTCTTCTGGCCAACCTATTGATGTTT 1884  
DB 530 ATGCGTTTGAATGCGCTTACCTACTTTGGCCAACCTATCGGGGATTTACATTCAGAAAT 589  
QY 1885 GTATAGACATCACACTTTAACTTTTAACTTGTCTGTAGAGTGAATATCCATATTTA 1944  
DB 590 ATACATGACTTCAACCATATTAACCCCTTTTGTGAAGTAACTGAATGTTTCATATTTA 649

Oy		1945	ATGCTTAGTTT	TAGTGCTC	TATTATCGATCATCT	1977
D <sub>b</sub>		650	ATGTGGGT	TAGTGTTTTT	AAC TGATTAT	682

## RESULT 4

```

US-09-678-300-12
: Sequence 12, Application US/09678300
: Patent No. 6420548
: GENERAL INFORMATION:
: APPLICANT: VOZINA, Marc-Andr,
: APPLICANT: MEDICAGO INC.
: TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
: FILE REFERENCE: 14149-3*PCT*
: CURRENT APPLICATION NUMBER: US/09/678,300
: CURRENT FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US 60/157,133
: PRIOR FILING DATE: 1999-10-04
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 12
: LENGTH: 2232
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Sequences to be used as promoter for r
: OTHER INFORMATION: expression of foreign genes
US-09-678-300-12

```

## RESULT 5

```

US-09-678-300-2
; Sequence 2, Application US/09678300
; Patent No. 6420548
; GENERAL INFORMATION:
; APPLICANT: VOZINA, Louis-Philippe
; APPLICANT: D'ACUST, Marc-Andr.
; APPLICANT: MEDICAGO INC.
; TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
; FILE REFERENCE: 14149-3"PCT"
; CURRENT APPLICATION NUMBER: US/09/678,300
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/157,133
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2808
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequences to be used as promoter for regulating
; OTHER INFORMATION: expression of foreign genes
US-09-678-300-2

```

APPLICANT: MEDICAGO INC.  
TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF  
FILE REFERENCE: 14149-3\*PCT\*  
CURRENT APPLICATION NUMBER: US/09/678,300  
CURRENT FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: US 60/157,133  
PRIOR FILING DATE: 1999-10-04  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 2863  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sequences to be used as promoter for regulating  
expression of foreign genes  
US-09-678-300-5

Query Match 9.5% Score 209.4; DB 4; Length 2863;  
Best Local Similarity 66.5%; Pred. No. 3.5e-51;  
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGAAGGCTGCTGTTTGAAGTTACATCC 1545  
DB 909 AGATCTAGCAATTTAACTCTGAGCTCTTCAAGACTGCTGTTTACGAAGTTACGTC 968  
QY 1546 CTGAATCTGCTGCTGATGAAGCTGAAAGCCCTGAAGTTATAGAGGGGGAGTCT 1605  
DB 969 CTGAATCATGCTCTGATGAAGCCCTGAAAGACCTCAATTTCTAAAGGTGGCGATAA 1028  
QY 1606 TTAAGACTCTACAAATATACCAATTTGGCTTGACACAGACAGAGCTCTTTATACCTTC 1665  
DB 1029 TTGAAGTTTACAAATATATACCTGCGGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1088  
QY 1666 AGCTTCAAGGTGATGCTGATTTGAGGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1725  
DB 1089 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAGCAATCTTGTGCCAAGTTT 1148  
QY 1726 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGCTACCTCTGCTACCTGAAAT 1778  
DB 1149 GAAGTAATTTTGTGAGCATATGTTGAGCTACCTACCAATTTACATGATCAGTACGAT 1208  
QY 1779 AGCTTCACCTAGCTGAGCAGTACGATAGTTTGAAGATGAGTATGGCAGTGAATATGGC 1838  
DB 1209 AGCTCTTCACTTAAGTGAAGATGAAGTTTGAAGATGAGTATGACCATGGAGTCGCGC 1268  
QY 1839 ATGCGTT-----TATTATGCTAGTTTCTTGGCCAACTCATCGGGATTTACATTCAGAAA 1884  
DB 1269 ATGCGTTTGTAAATGCTTACCTTCTTGGCCAACTCATCGGGATTTACATTCAGAAA 1328  
QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTGTCTGTAGAGTGCAATCCATATTTA 1944  
DB 1329 ATACATGACTCAACCATCTTAAACCCCTTTTGTGAAGTAACTGAATGTTTCATATTTA 1388  
QY 1945 ATGCTAGTTTATGCTCTTATCTGATCATCT 1977  
DB 1389 ATGTTGGGTTGAGTGTGTTTACTTGCATATAT 1421

RESULT 7  
US-09-678-300-8  
Sequence 8, Application US/09678300  
Patent No. 6420548  
GENERAL INFORMATION:  
APPLICANT: VOZINA, Louis-Philippe  
APPLICANT: D'Aoust, Marc-Andre,  
APPLICANT: MEDICAGO INC.  
TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF  
FILE REFERENCE: 14149-3\*PCT\*  
CURRENT APPLICATION NUMBER: US/09/678,300  
CURRENT FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: US 60/157,133  
PRIOR FILING DATE: 1999-10-04  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 11  
LENGTH: 2971

PRIOR APPLICATION NUMBER: US 60/157,133  
PRIOR FILING DATE: 1999-10-04  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 2904  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sequences to be used as promoter for regulating  
expression of foreign genes  
US-09-678-300-8

Query Match 9.5% Score 209.4; DB 4; Length 2904;  
Best Local Similarity 66.5%; Pred. No. 3.5e-51;  
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGATGAAGCTGCTGTTTGAAGTTACATCC 1545  
DB 909 AGATCTAGCAATTTAACTCTGAGCTCTTCAAGACTGCTGTTTACGAAGTTACGTC 968  
QY 1546 CTGAATCTGCTGCTGATGAAGCTGAAAGCCCTGAAAGACCTCAATTTCTAAAGGTGGCGATAA 1605  
DB 969 CTGAATCATGCTCTGATGAAGCCCTGAAAGACCTCAATTTCTAAAGGTGGCGATAA 1028  
QY 1606 TTAAGACTCTACAAATATACCAATTTGGCTTGACACAGACAGAGCTCTTTATACCTTC 1665  
DB 1029 TTGAAGTTTACAAATATATACCTGCGGGCTTGACACAGAGCAAGCTCTTTATACCTTC 1088  
QY 1666 AGCTTCAAGGTGATGCTGATTTGAGGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1725  
DB 1089 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAGCAATCTTGTGCCAAGTTT 1148  
QY 1726 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGCTACCTCTGCTACCTGAAAT 1778  
DB 1149 GAAGTAATTTTGTGAGCATATGTTGAGCTACCTACCAATTTACATGATCAGTACGAT 1208  
QY 1779 AGCTTCACCTAGCTGAGCAGTACGATAGTTTGAAGATGAGTATGGCAGTGAATATGGC 1838  
DB 1209 AGCTCTTCACTTAAGTGAAGATGAAGTTTGAAGATGAGTATGACCATGGAGTCGCGC 1268  
QY 1839 ATGCGTT-----TATTATGCTAGTTTCTTGGCCAACTCATCGGGATTTACATTCAGAAA 1884  
DB 1269 ATGCGTTTGTAAATGCTTACCTTCTTGGCCAACTCATCGGGATTTACATTCAGAAA 1328  
QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTGTCTGTAGAGTGCAATCCATATTTA 1944  
DB 1329 ATACATGACTCAACCATCTTAAACCCCTTTTGTGAAGTAACTGAATGTTTCATATTTA 1388  
QY 1945 ATGCTAGTTTATGCTCTTATCTGATCATCT 1977  
DB 1389 ATGTTGGGTTGAGTGTGTTTACTTGCATATAT 1421

RESULT 8  
US-09-678-300-11  
Sequence 11, Application US/09678300  
Patent No. 6420548  
GENERAL INFORMATION:  
APPLICANT: VOZINA, Louis-Philippe  
APPLICANT: D'Aoust, Marc-Andre,  
APPLICANT: MEDICAGO INC.  
TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF  
FILE REFERENCE: 14149-3\*PCT\*  
CURRENT APPLICATION NUMBER: US/09/678,300  
CURRENT FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: US 60/157,133  
PRIOR FILING DATE: 1999-10-04  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 11  
LENGTH: 2971

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: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Sequences to be used as promoter for regulating
: OTHER INFORMATION: expression of foreign genes
: US-09-678-300-11

Query Match          9.5%; Score 209.4; DB 4; Length 2971;
Best Local Similarity 66.5%; Pred. No. 3.5e-51;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGGAAGGCTCTCTGTTTGAAGTTTCAACATCC 1545
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 909 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTTACGAAGTTTCAAGTCC 968

QY 1546 CTGAATCTTGCTGCTGATGGAAGCTGAAAGCCCTGAAGTTTATAAGAGGGGGAGTCT 1605
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 969 CTGAATCATGTTCTGATGGAAGCCCTGAAGACTCTCAAAATTTCTAAAGGTGGCGATAA 1028

QY 1606 TTAAGAACTCTACAAATATACCCATTTGCTGACAGAGCAAGCTCTTTATACCTTC 1665
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1029 TTGAAGGTTTACAAATATACCTCGCGGCTTGACAGAGGCAAGCTCTTTATACCTTC 1088

QY 1666 AGCTTCAAGGTTGATGCTGATTTGAGGAGTCACTTGAGAGCAATCTTTGTGCCAAGTTT 1725
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1089 CAGTTCAACGGGGATGTTGATTTTCAAGAGTCACTTGAGAGCAATCTTTGTGCCAAGTTT 1148

QY 1726 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGGTACCTCTGCTACCTGAAT 1778
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1149 GAAGTAATTTTGTGAGCATATGTTGAGTACCTACATAATTTACATGATCACTGACAT 1208

QY 1779 AGCTTCACTTACCTAGTACGACATAGAGTTTGTAGGAATGAGTATGCGAGTGAATATGCC 1838
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1209 AGCTTCACTTACCTAGTACGACATAGAGTTTGTAGGAATGAGTATGCGAGTGAATATGCC 1268

QY 1839 ATGGCTT-----TATTTATGCTAGTTTCTTGCCCACTCATCGGGATTTACATTCAGAAAAT 1884
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1269 ATGGCTTGTAAAGCTACCTACTTTGGCCCACTCATCGGGATTTACATTCAGAAAAT 1328

QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTTGTTCTGTAGAAAGTGAATATCCATATTTA 1944
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGATAACTGAATGTTTATATTTA 1388

QY 1945 ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT 1977
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1389 ATGTTGGTTGTAGTCTTTTACTTGATTAT 1421

RESULT 10
US-08-737-524B-1
: Sequence 1, Application US/08737524B
: Patent No. 5912414
: GENERAL INFORMATION:
: APPLICANT: CARL SAVERIO FALCO
: APPLICANT: DOMINICK ANTHONY GUIDA, JR.
: APPLICANT: MARY ELIZABETH HARNETT LOCKE
: TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS, CHIMERIC
: TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
: TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEEDS
: TITLE OF INVENTION: OF PLANTS
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
: STREET: 1007 MARKET STREET
: CITY: WILMINGTON
: STATE: DELAWARE
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 19898
: COMPUTER READABLE FORM:
: MEDIUM TYPE: DISKETTE, 3.50 INCH
: OPERATING SYSTEM: MICROSOFT WINDOWS 95
: SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/737,524B
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: LYNNE M. CHRISTENBURY
```





CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/S-30306/A/CGC1976  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 937:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 665 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE: PAG1581RP  
US-08-998-416-937

Query Match 1.9% Score 42.4; DB 4; Length 665;  
Best Local Similarity 46.9%; Pred. No. 0.013;  
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;  
QY 1845 TTATTTATGCTAGTTCTTGGCCCACTCATGATGTTTGTATAGACATCACACTTTA 1904  
DB 196 TTGATTATTTATCTATTAACATAAAACATTTTAAATGTTTATAAATAAAGAAATTA 255  
QY 1905 ATTTAAACTGTTCTGTAGAGTGCATATTTTAAATGTTTGTATAGTGTCT 1964  
DB 256 CTATAGAAATATTTTAAATAGTATTTTAAATTTAAATTTAAATATACCATTTT 314  
QY 1965 TATCTGATCATCTAGAGTGCATGTTTGTATATTTGAGTGAACCTCAATCTAATA 2024  
DB 315 TATTATAATAGATTTAAGTTTATTAATTAAGTATATATTAATTTATATA 374  
QY 2025 GAAGGATCAGATGTTTCACTCAAGACATTTATTTACTTCATGTTGTTTGTATGATCTCGA 2084  
DB 375 AATTATTTAATTTACTTCATGATATATATAATTTAAATGTTACCTTTTCAATATTTTA 434  
QY 2085 GCTTTTATAGTCTGGAAGTCTCCCTGTGTTGAGCACCTGTTTATGCTTCAGTGTTA 2144  
DB 435 TTTTATAGTCTAGTATATTTCTTATTTAATAGTCTACCTTTTAAATGATATTACTAC 494  
QY 2145 CTGTCAGTGGTATCGTTTGTACCTCTAAATAAAAAAAAAAAAAAAAAAAAAA 2196  
DB 495 CTACTAAATATTTACTTAATAATATATTTAATTAAGAAATCTTAAATCTAATAA 546

RESULT 13  
US-08-998-416-701  
Sequence 701, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jurgen  
APPLICANT: Knechtle, Philipp  
APPLICANT: Reibschung, Corinne  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patencin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/998,416  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CH 0016/97  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/S-30306/A/CGC1976  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 701:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 701 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE: PAG1462RP  
US-08-998-416-701

Query Match 1.9% Score 42.4; DB 4; Length 701;  
Best Local Similarity 46.9%; Pred. No. 0.014;  
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;  
QY 1845 TTATTTATGCTAGTTCTTGGCCCACTCATGATGTTTGTATAGACATCACACTTTA 1904  
DB 196 TTGATTATTTATCTATTAACATAAAACATTTTAAATGTTTATAAATAAAGAAATTA 255  
QY 1905 ATTTAAACTGTTCTGTAGAGTGCATATTTTAAATGTTTGTATAGTGTCT 1964  
DB 256 CTATAGAAATATTTTAAATAGTATTTTAAATTTAAATTTAAATATACCATTTT 314  
QY 1965 TATCTGATCATCTAGAGTGCATGTTTGTATATTTGAGTGAACCTCAATCTAATA 2024  
DB 315 TATTATAATAGATTTAAGTTTATTAATTAAGTATATATTAATTTATATA 374  
QY 2025 GAAGGATCAGATGTTTCACTCAAGACATTTATTTACTTCATGTTGTTTGTATGATCTCGA 2084  
DB 375 AATTATTTAATTTACTTCATGATATATATAATTTAAATGTTACCTTTTCAATATTTTA 434  
QY 2085 GCTTTTATAGTCTGGAAGTCTCCCTGTGTTGAGCACCTGTTTATGCTTCAGTGTTA 2144  
DB 435 TTTTATAGTCTAGTATATTTCTTATTTAATAGTCTACCTTTTAAATGATATTACTAC 494  
QY 2145 CTGTCAGTGGTATCGTTTGTACCTCTAAATAAAAAAAAAAAAAAAAAAAAAA 2196  
DB 495 CTACTAAATATTTACTTAATAATATATTTAATTAAGAAATCTTAAATCTAATAA 546

RESULT 14  
US-08-998-416-786  
Sequence 786, Application US/08998416  
Patent No. 6239264  
GENERAL INFORMATION:  
APPLICANT: Philippsen, Peter  
APPLICANT: Pohlmann, Rainer  
APPLICANT: Steiner, Sabine  
APPLICANT: Mohr, Christine  
APPLICANT: Wendland, Jurgen  
APPLICANT: Knechtle, Philipp  
APPLICANT: Reibschung, Corinne  
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII  
NUMBER OF SEQUENCES: 1152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6239264artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6239264th Carolina  
COUNTRY: USA  
ZIP: 27709



Search completed: April 28, 2003, 03:45:53  
Job time : 157 secs

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 01:14:21 : Search time 239 Seconds  
(without alignments)  
10007.142 Million cell updates/sec

Title: US-09-913-858A-1  
Perfect score: 2198  
Sequence: 1 actaactcaacgctgatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	84.2	3.8	287	10	US-09-294-093B-5780
2	83.4	3.8	277	10	US-09-578-574-7836
3	49.2	2.2	477	9	US-09-918-995-2051
4	41.2	1.9	1373	10	US-09-960-352-12673
5	41	1.9	1373	10	US-09-925-301-133
6	41	1.9	4065	10	US-09-925-302-245
7	40.2	1.8	1184	9	US-10-123-155-412
8	40.2	1.8	1942	10	US-09-731-872-43
9	39	1.8	1446	10	US-09-764-853-180
10	39	1.8	1446	10	US-09-764-853-370
11	38.8	1.8	2523	10	US-09-861-451A-29
12	38.6	1.8	873	10	US-09-770-445-553
13	38.2	1.7	386	10	US-09-770-791-77
14	38.2	1.7	473	10	US-09-960-352-6407
15	38	1.7	345	10	US-09-770-791-772
16	38	1.7	4298	9	US-09-997-672-1
17	38	1.7	4921	9	US-09-997-672-2
18	37.8	1.7	375	10	US-09-960-352-15014
19	37.8	1.7	413	10	US-09-924-035A-435

20	37.8	1.7	1566	10	US-09-974-300-1166
21	37.8	1.7	1613	10	US-09-745-763-78
22	37.6	1.7	1435	10	US-09-732-618-15
23	37.6	1.7	2022	9	US-09-955-999-56
24	37.6	1.7	2756	9	US-09-963-234-1
25	37.4	1.7	617	10	US-09-764-877-121
26	37.4	1.7	812	10	US-09-770-445-770
27	37.4	1.7	1079	10	US-09-770-445-126
28	37.4	1.7	1461	9	US-10-080-960-3
29	37.4	1.7	1669	9	US-10-080-960-1
30	37.4	1.7	1947	10	US-09-864-761-4439
31	37	1.7	277	10	US-09-980-352-12673
32	37	1.7	418	9	US-09-918-995-7350
33	37	1.7	2290	10	US-09-822-849A-152
34	36.8	1.7	215	10	US-09-960-352-5093
35	36.8	1.7	500	9	US-09-918-995-23879
36	36.8	1.7	1024	9	US-10-123-155-198
37	36.8	1.7	1058	10	US-09-452-239-11
38	36.6	1.7	431	10	US-09-960-352-5558
39	36.6	1.7	689	9	US-10-001-883-3
40	36.6	1.7	2000	9	US-09-938-842A-3564
41	36.6	1.7	2000	10	US-09-887-576-112
42	36.4	1.7	308	10	US-09-960-352-7670
43	36.2	1.6	193	10	US-09-867-701-9750
44	36.2	1.6	257	10	US-09-887-576-609
45	36.2	1.6	1401	10	US-09-925-301-410

ALIGNMENTS

RESULT 1

US-09-294-093B-5780  
: Sequence 5780, Application US/09294093B  
: Patent No. US20010051335A1  
: GENERAL INFORMATION:  
: APPLICANT: Lalgudi, Raghunath, V.  
: APPLICANT: Ito, Laura, Y.  
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL  
: FILE REFERENCE: PL-0009 US  
: CURRENT APPLICATION NUMBER: US/09/294, 093B  
: CURRENT FILING DATE: 1999-04-16  
: PRIOR APPLICATION NUMBER: 60/082,567  
: PRIOR FILING DATE: April 21, 1998  
: NUMBER OF SEQ ID NOS: 6207  
: SOFTWARE: PERL Program  
: SEQ ID NO 5780  
: LENGTH: 287  
: TYPE: DNA  
: ORGANISM: Zea mays  
: FEATURE:  
: NAME/KEY: misc\_feature  
: OTHER INFORMATION: Incyte ID No. US20010051335A1 700382332H1

Query Match 3.8%; Score 84.2; DB 10;  
Best Local Similarity 67.2%; Pred. No. 1.5e-13;  
Matches 119; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy	658	GCATTTCGGTTACTTCACCAAGTGAACAGTAGCATCTCGGATCAATCGATCAGCA 717
Db	39	GGATCGGATTAATGTCATATCTTCTGTAGAGGGTATCTTCGGATCAATCGATCATCT 98
Qy	718	GAATCATATGCTGCAACAAATATGCGATGGCAAGAGGGGATATACATGCTGAATG 777
Db	99	CAATATTATTCAAGAATAGTATTGATGCTGCGAGGAGGAGGATCAAGATTGTGATG 158
Qy	778	ACAACCACTATCTTCGGATGTCCTGCTGTGATATTTTCATGGCTGACTGAT 834
Db	159	ACATACAGCCTTTCTTCACACAGTCCAGTTGGCTACTCTTCATGGGCTGAATGAT 215



Db 789 NPRAMGRFSDVITGPGACVPACFDDOSPDAYSAYVLASLAGELQAVESSEKPNPNAIG 848  
Oy 1482 CCTGAGGTCTAGCAATTAACCTGTAATGCTGTGAAGCGTGTGTTGTTTGAAGTTCCAC 1541  
Db 849 VPQPLNKLNVRRDHDPRVKNTAFQISMAKPRPNSAESNGPIYAFENLRACEAPP 908  
Oy 1542 A 1542  
Db 909 A 909  
RESULT 8  
US-09-731-872-43  
: Sequence 43, Application US/09731872  
: Patent No. US20020102604A1  
: GENERAL INFORMATION:  
: APPLICANT: Dumas Milne Edwards, Jean Baptiste  
: APPLICANT: Bouqueleret, Lydie  
: APPLICANT: Jobert, Severin  
: TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS  
: FILE REFERENCE: 78.053.REG  
: CURRENT FILING DATE: 2000-12-07  
: PRIOR APPLICATION NUMBER: US/09/731,872  
: PRIOR FILING DATE: 2000-12-07  
: PRIOR APPLICATION NUMBER: US 60/169,629  
: PRIOR FILING DATE: 1999-12-08  
: PRIOR APPLICATION NUMBER: US 60/187,470  
: NUMBER OF SEQ ID NOS: 482  
: SOFTWARE: Patent.pm  
: SEQ ID NO 43  
: LENGTH: 1942  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: NAME/KEY: CDS  
: LOCATION: 334..1551  
: NAME/KEY: sig.peptide  
: LOCATION: 334..426  
: OTHER INFORMATION: Von Heijne matrix  
: OTHER INFORMATION: score 4.0554926521937  
: OTHER INFORMATION: seq TVFLVTLQALDT/VE  
US-09-731-872-43

Query Match 1.8%; Score 40.2; DB 10; Length 1942;  
Best Local Similarity 47.1%; Pred. No. 1.5;  
Matches 123; Conservative 0; Mismatches 138; Indels 0; Gaps 0;  
Oy 1021 CACTACAAATTTAGCTTAGCTTTGAAATTCGAATGAGGAGATTTATGTAACGAAAAA 1080  
Db 1276 CAGTATAAGTTTATCTAGCTTTTGAGATGCGAGTTTGTGATGACTACATCAGTGAAG 1335  
Oy 1081 TTCTTCCAAATCCCTTTGCTGGAACCTGCCCTGTGTTGTTGGTGTCCAAATATTTCAG 1140  
Db 1336 TTCTGGAGGCACTGAAACCTGGGGAGTCCCTGTATATTACGATCCCCCAGCATCACA 1395  
Oy 1141 GACTTCTCCTCTCTCTCTCTCAATTTTACATATTAAGAGATAGAGGATGTTGAGTCT 1200  
Db 1396 GACTGCTGCTCAAGTAACAAAGTGTCTTCTTGTATCAGAAATTTCTCACCCAGGAA 1455  
Oy 1201 GTTCCAAAGCAATGAGATATCTACGAAATCCGGAAGCATATATCAATCATTCAGG 1260  
Db 1456 CTGCAAGTTACATCAGACACTGGATTCTGATGACAGATTGTATGAGGCGCTATGTAGAA 1515  
Oy 1261 TGAAGATGAGGCTCCATCT 1281  
Db 1516 TGAAGCTGAAGGTAGATCT 1536

RESULT 9  
US-09-764-853-180  
: Sequence 180, Application US/09764853  
: Patent No. US20020090672A1  
: GENERAL INFORMATION:

: APPLICANT: Rosen et al.  
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
: FILE REFERENCE: P3206  
: CURRENT APPLICATION NUMBER: US/09/764,853  
: CURRENT FILING DATE: 2001-01-17  
: Prior application data removed - consult PALM or file wrapper  
: NUMBER OF SEQ ID NOS: 939  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 180  
: LENGTH: 1446  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: NAME/KEY: SITE  
: LOCATION: (1446)  
: OTHER INFORMATION: n equals a.t.g. or c  
US-09-764-853-180

Query Match 1.8%; Score 39; DB 10; Length 1446;  
Best Local Similarity 49.3%; Pred. No. 2.7;  
Matches 99; Conservative 1; Mismatches 101; Indels 0; Gaps 0;  
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Oy 2058 TACTTCATGTTGTTTGTGATGATCTCGAGCTTTTATAGTCTGGAACCTGTCCTGTGGTT 2117  
Db 1298 TTCATTGGAATAAATACTACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1357  
Oy 2118 TGAGCACCTGTTTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2177  
Db 1358 CAAGTACCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1417  
Oy 2178 AAAAAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 2198  
Db 1418 AAAAAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1438

RESULT 10  
US-09-764-853-370/c  
: Sequence 370, Application US/09764853  
: Patent No. US20020090672A1  
: GENERAL INFORMATION:  
: APPLICANT: Rosen et al.  
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
: FILE REFERENCE: P3206  
: CURRENT APPLICATION NUMBER: US/09/764,853  
: CURRENT FILING DATE: 2001-01-17  
: Prior application data removed - consult PALM or file wrapper  
: NUMBER OF SEQ ID NOS: 939  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 370  
: LENGTH: 1446  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: NAME/KEY: SITE  
: LOCATION: (1)  
: OTHER INFORMATION: n equals a.t.g. or c  
US-09-764-853-370

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Best Local Similarity 49.3%; Pred. No. 2.7;  
Matches 99; Conservative 1; Mismatches 101; Indels 0; Gaps 0;  
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Oy 2058 TACTTCATGTTGTTTGTGATGATCTCGAGCTTTTATAGTCTGGAACCTGTCCTGTGGTT 2117  
Db 149 TTCATTGGAATAAATACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 90







GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 00:45:31 : Search time, 5603 seconds  
(without alignments)  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

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4: gb.om.\*  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2198	100.0	2198	6	AX033383	AX033383 Sequence
2	2191.6	99.7	2198	8	VRA18529	Y18529 Vigna radia
3	690	31.4	1506	8	ATH404860	AJ404860 Arabidops
4	690	31.4	1729	8	ATH345084	AJ345084 Arabidops
5	678.8	30.9	1542	8	ATH345085	AJ345085 Arabidops
6	678.8	30.9	1938	8	AY054522	AY054522 Arabidops
7	664.8	20.2	1824	8	ATH404861	AJ404861 Arabidops
8	534	24.3	658	8	MTR416755	AJ416755 Medicago
9	349	15.9	787	8	AF277228	AF277228 Arabidops
10	346	15.7	588	8	AF277229	AF277229 Arabidops
11	209.4	9.5	2069	6	AX105537	AX105537 Sequence
12	209.4	9.5	2124	6	AX105540	AX105540 Sequence
13	209.4	9.5	2165	6	AX105543	AX105543 Sequence
14	209.4	9.5	2232	6	AX105546	AX105546 Sequence
15	209.4	9.5	2208	6	AX105536	AX105536 Sequence
16	209.4	9.5	2883	6	AX105539	AX105539 Sequence
17	209.4	9.5	2904	6	AX105542	AX105542 Sequence
18	209.4	9.5	2971	6	AX105545	AX105545 Sequence
19	209.4	9.5	3714	6	AX105535	AX105535 Sequence
20	178.8	8.1	104679	8	AC011807	AC011807 Arabidops
21	171	7.8	81875	8	AP000419	AP000419 Arabidops
22	155	7.1	89134	2	AP004162	AP004162 Oryza sat
23	155	7.1	141717	2	AP004457	AP004457 Oryza sat
24	105	4.8	105	6	AX033385	AX033385 Sequence
25	60.2	2.7	1449	8	BVU315848	AJ315848 Beta vulg
26	60	2.7	1630	8	LES313193	AJ313193 Lycopersi
27	54.6	2.5	177674	2	AC127920	AC127920 Rattus no
28	54.6	2.5	190304	2	AC114439	AC114439 Rattus no
29	53.4	2.4	97683	2	AC116548	AC116548 Dictyoste
30	53.4	2.4	234488	2	AC109698	AC109698 Rattus no
31	53	2.4	807	8	MTR416757	AJ416757 Medicago
32	51.8	2.4	188464	9	AC096757	AC096757 Homo sapi
33	50.6	2.3	122160	2	CNS074PV	AL731761 Oryza sat
34	50	2.3	1149	3	CEL505020	AJ505020 Caenorhab
35	50	2.3	39370	3	AC006674	AC006674 Caenorhab
36	50	2.3	180664	2	AC006706	AC006706 Caenorhab
37	50	2.3	183800	2	AC123118	AC123118 Rattus no
38	49.8	2.3	11109	2	AC121599	AC121599 Mus muscu
39	49.6	2.3	1128	10	AF345993	AF345993 Rattus no
40	49.4	2.2	1182	8	AY026941	AY026941 Arabidops
41	49.4	2.2	1209	8	ATH404862	AJ404862 Arabidops
42	49.4	2.2	56956	2	AC117081	AC117081 Dictyoste
43	49.4	2.2	80413	8	AC021665	AC021665 Arabidops
44	49.2	2.2	1479	6	AX356085	AX356085 Sequence
45	49.2	2.2	2408	9	AK095482	AK095482 Homo sapi

ALIGNMENTS

RESULT 1	AX033383	Sequence 1 from Patent WO0049153.	2198 bp	DNA	linear	PAT 21-SEP-2000
AX033383	LOCUS	AX033383				
DEFINITION	AX033383	Sequence 1 from Patent WO0049153.				
ACCESSION	AX033383	AX033383.1	GI:10280157			
VERSION	AX033383.1	GI:10280157				
KEYWORDS		unidentified.				
SOURCE		unclassified.				
ORGANISM		unclassified.				
REFERENCE		1 (bases 1 to 2198)				
AUTHORS		Altman, F.				
TITLE		Fucosyl transferase gene				
JOURNAL		Patent: WO 0049153-A.1 24-AUG-2000;				
		ALTMANN FRIEDRICH (AT)				

FEATURES		Location/Qualifiers									
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ORIGIN											
Query Match	100.0%	Score 2198:	DB 6:	Length 2198;							
Best Local Similarity	100.0%	Pred. No. 0:									
Matches 2198;	Conservative 0:	Mismatches 0:	Indels 0:	Gaps							
QY 1	ACTAACTCAACGCTGCATTTCTCTTTTCTTCAGGGAAACATCCACCCATAACAACAA 60										
DB 1	ACTAACTCAACGCTGCATTTCTCTTTTCTTCAGGGAAACATCCACCCATAACAACAA 60										
QY 61	AAAAACACACGACGAGCTGTGTGTGTGTATCGTCTCTTTTCTTAAACAGCACCCCA 120										
DB 61	AAAAACACACGACGAGCTGTGTGTGTATCGTCTCTTTTCTTAAACAGCACCCCA 120										
QY 121	TCATGGAATCGTGTCTATAACGCCAAATTTTCCATTCCTCTTGATTTTATTATTT 180										
DB 121	TCATGGAATCGTGTCTATAACGCCAAATTTTCCATTCCTCTTGATTTTATTATTT 180										
QY 181	TCGGGAATGGGAGTTGGGGGGCGAATGAATGATGGGTCTGTGACGAATCTTCGAGGC 240										
DB 181	TCGGGAATGGGAGTTGGGGGGCGAATGAATGATGGGTCTGTGACGAATCTTCGAGGC 240										
QY 241	TCGAGAACAGATGGTGGCCAAACAGACAGTTACCCGTTTTGGGTCGGGAGGCAACCCA 300										
DB 241	TCGAGAACAGATGGTGGCCAAACAGACAGTTACCCGTTTTGGGTCGGGAGGCAACCCA 300										
QY 301	AAGAGGAATGGAGCAATCTAATGCCTCTGTGTGTGGCCCTGTGGTCNTCGGGAGATC 360										
DB 301	AAGAGGAATGGAGCAATCTAATGCCTCTGTGTGTGGCCCTGTGGTCNTCGGGAGATC 360										
QY 361	GGGTTCTCGGTAGTGGATATGGCCAAACAGCGGCCATGGTGTGACTCCCTCGCTGAC 420										
DB 361	GGGTTCTCGGTAGTGGATATGGCCAAACAGCGGCCATGGTGTGACTCCCTCGCTGAC 420										
QY 421	TTCTTCTACCGCTCTCGAGCGGCTGTGTAAGGTGCAGATTTGGGGTTGGGTTCGTGGCT 480										
DB 421	TTCTTCTACCGCTCTCGAGCGGCTGTGTAAGGTGCAGATTTGGGGTTGGGTTCGTGGCT 480										
QY 481	TCGTATCGGAATCTCGAATCGTATAGTGTGAGGAATGGTTCGAGAGGGAGGATGCTGTC 540										
DB 481	TCGTATCGGAATCTCGAATCGTATAGTGTGAGGAATGGTTCGAGAGGGAGGATGCTGTC 540										
QY 541	ACGTATTCGAGGGGCTTTCCAAAGAGCCTATTTTTGTTCCTGGAGCTGATCAGGAGTGG 600										
DB 541	ACGTATTCGAGGGGCTTTCCAAAGAGCCTATTTTTGTTCCTGGAGCTGATCAGGAGTGG 600										
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DB 601	AAGTCGTCTCGGTGGATGTAAATTTGGGTTTATGTGGGGATAGAAAGCCAGATGCCCA 660										
QY 661	TTTGGGTTACCTCAACCACTGCAACAGCTAGCATTCTGCCATCAATGGATCAGCAGAA 720										
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QY 721	TACTATGCTGAGAACAAATATGGCCATGGCAACGAGGGGATATAACATCGTAATGACA 780										
DB 721	TACTATGCTGAGAACAAATATGGCCATGGCAACGAGGGGATATAACATCGTAATGACA 780										
QY 781	ACCAGTCTATCTCCGGATGTTCTGTGTGGATATTTTTCATGGCTGAGTATGATATGATG 840										
DB 781	ACCAGTCTATCTCCGGATGTTCTGTGTGGATATTTTTCATGGCTGAGTATGATATGATG 840										
QY 841	GCACAGTGCACGCGAAACATGAAGTGTCTTTGCAGCTGCTTTTCATTTCCAAATGTGGT 900										
DB 841	GCACAGTGCACGCGAAACATGAAGTGTCTTTGCAGCTGCTTTTCATTTCCAAATGTGGT 900										
QY 901	GCTCGAAATTTCCGGTTCGAGCTCTTTGAGCGCCCTTGAANAATCAAAACATCAAAATTTGAT 960										

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Db 1981 AGTCACAGCTTCTGTATATTGTGAGTGAAACTGAATCTAATAGAGGATCAGATGTTT 2040
Qy 2041 CACTCAAGACACATPATTACTTCATGTGTGTTTGTATGATCGAGCTTTTATAGTCTCG 2100
Db 2041 CACTCAAGACACATPATTACTTCATGTGTGTTTGTATGATCGAGCTTTTATAGTCTCG 2100
Qy 2101 GAACTGTCTCTGTGTGTGACACCTGTTATTGCTTCAGTGTACTGTCCAGTGGTTATC 2160
Db 2101 GAACTGTCTCTGTGTGTGACACCTGTTATTGCTTCAGTGTACTGTCCAGTGGTTATC 2160
Qy 2161 GTTTTGACCTCTAAAAAATAAAAAAAAAAAAAAAAAAAAAA 2198
Db 2161 GTTTTGACCTCTAAAAAATAAAAAAAAAAAAAAAAAAAAAA 2198

RESULT 2
VRA18529
LOCUS      VRA18529          2198 bp      mRNA      linear      PLN 01-NOV-2001
DEFINITION Vigna radiata mRNA for alpha-1,3-fucosyltransferase (Fuct c3).
ACCESSION  Y18529
VERSION     Y18529.1 GI:5702038
KEYWORDS   alpha-1,3-fucosyltransferase; fuct gene; GDP-L-Fuc.
SOURCE      mung bean.
ORGANISM   Vigna radiata var. radiata
REFERENCE  1
AUTHORS    Leiter,H., Mucha,J., Staudacher,E., Grimm,R., Glossl,J. and
            Altman,F.
TITLE      Purification, cDNA cloning, and expression of GDP-L-Fuc:Asn-linked
            GlcNAc alpha1,3-fucosyltransferase from mung beans
JOURNAL    J. Biol. Chem. 274 (31), 21830-21839 (1999)
MEDLINE    99348317
PUBMED     10419500
REFERENCE  2 (bases 1 to 2198)
AUTHORS    Mucha,J.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-1998) J. Mucha, Institut fuer Chemie, Universitaet
            fuer Bodenkultur Wien, Muthgasse 18, 1190 Wien, Austria
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LOCUS			
1729 bp mRNA linear PLN 20-SEP-2001			

DEFINITION	Arabidopsis thaliana mRNA for core-alpha,3-fucosyltransferase 1 (fuct1 gene).		
ACCESSION	AJ345084		
VERSION	AJ345084.1		
KEYWORDS	core-alpha,3-fucosyltransferase 1; fuct1 gene.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
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REFERENCE	1 (bases 1 to 1729)		
AUTHORS	Bakker, H.		
TITLE	Molecular cloning and characterization of a plant (Beta vulgaris)alpha,4-fucosyltransferase with specificity for Lewis		
JOURNAL	and Lewisb synthesis		
REFERENCE	2 (bases 1 to 1729)		
AUTHORS	Bakker, H.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-SEP-2001) Bakker H., Plant Research International,		
	Wageningen University and Research centre, droevendaalsesteeg 1,		
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 DEFINITION Arabidopsis thaliana mRNA for core-alpha.1.3fucosyltransferase 2  
 (fuc2 gene).  
 ACCESSION AJ345085  
 VERSION AJ345085.1 GI:15722481

KEYWORDS core-alpha.1.3fucosyltransferase 2; fucT2 gene.  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 REFERENCE 1 (bases 1 to 1542)  
 AUTHORS Bakker, H.  
 TITLE Molecular cloning and characterization of a plant (Beta vulgaris) alpha.1.4-fucosyltransferase with specificity for Lewis x  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1542)  
 AUTHORS Bakker, H.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-SEP-2001) Bakker H., Plant Research International,  
 Wageningen University and Research center, droevendaalsesteeg 1,  
 Netherlands 6708PB, NETHERLANDS  
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LOCUS  
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ACCESSION  
AY054522  
VERSION  
AY054522.1 GI:15450883  
KEYWORDS  
FUT CDNA.  
SOURCE  
Arabidopsis thaliana.  
ORGANISM  
Arabidopsis thaliana

1938 bp mRNA linear PLN 05-SEP-2001

REFERENCE  
AUTHORS  
Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Mitende, M.,  
Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,  
Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,  
Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,  
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.,  
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.  
Direct Submission  
Submitted (28-AUG-2001) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA  
e-mail for correspondence: arabesequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL CDNA: "RIKEN  
Arabidopsis Full-Length cDNA"): Seki, N., Narusaka, M., Ishida, J.,  
Sato, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the  
sequencing and annotation of the RAFL cDNAs: Nguyen, M.,  
Southwick, A., Karlin-Neumann, G., Lam, B., Mizada, M., Palm, C.J.,  
Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K.,  
Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P.,  
Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.

Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed  
equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.  
(SSP/Stanford) contributed equally to this work as PIs.

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EVVV"









Db 722 AGCTAGCTTTTGAACAACCAACGAGGAGGATTATGTACAGAGAGAGTCTTCCAACT 781  
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Db 782 CTAGT 786

RESULT 10  
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DEFINITION partial cds.  
ACCESSION AF277229  
VERSION AF277229.1 GI:21628753  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 588)  
Kiefer-Meyer M.-C., Faye, L. and Gomord, V.  
Direct Submission  
Submitted (08-JUN-2002) LRI, CNRS UMR 6037, Faculte des Sciences,  
Universite de Rouen, Mont Saint Aignan 76821, France  
JOURNAL  
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Query Match 15.7%; Score 346; DB 8; Length 588;  
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Matches 436; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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ACCESSION AX105537  
VERSION AX105537.1 GI:13921581  
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SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 2069)  
AUTHORS v Zina, L.P. and D'Aoust, M.A.  
TITLE Method for regulating transcription of foreign genes in the  
presence of nitrogen  
JOURNAL Patent: WO 0125454-A 3 12-APR-2001;  
Medicago Inc. (CA)  
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Query Match 9.5%; Score 209.4; DB 6; Length 2069;  
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